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REFERENTE AUTHORS

Elkaryota; Hetazoa; Chordata; Craniata; Vertobrata; Eutoleostomi; Mandhallik; Eutheria; Primates; Catarrhini; Hodiniade; Homo. (Jases 1 to 1645)

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Into the exact sizes of the finished sequence that size is a size of the sequence.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 11, clone kPl1-780024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-APR-2000) Masahira Hattori, The Institute of Engel and Chemical Research (RIKEN), Genomic Sciences Center (GSC):
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Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homon
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BC021682.1 GI:18204950
Strausberg, R.
Direct Submission
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collect: amadanisystemsbiology.org
ALLy Malan, Jessica Fahey, Erin Helton,
Malan, Stephenie Rodrijues, Amy Sanchez
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Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Andradus
Madan, Stephanie Rodrigues, Amy Sancher and Michelie Wilting
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Contact: MGC help desk
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Homo sapiens DNA, clone:CMB9-6J10
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Hattori,M., Ishii,K., Toyoda,A., Taylor,I.L.
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Pujiyama,A., Yada,I., Totoki,Y., Watanabe,H. and Sukini,Y.,
Homo sapiens 121,922 genomic DNA of 11q12
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consists of 12 configs. The true order of the pieces is not known and their order in this sequence record is
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84627 54411; contig of 5485 bp in 1
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hes 77; Conserv
 ATAACTCCCAGAAGCTGCTGGTTCTATACAAACCCTTGGCCTGGAGCATASC 46_77
 Submitted (05-APR-2000) Masahira Huttori, The Institute of Professal and Chemical Research (RIKEN), Genomic Sciences Center (GSC) 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 250-0045 (Japan
 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Homo sapiens genomic DNA published only in Database (2000)

2 (bases 1 to 161582)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seug, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H.
 Homo sapiens genomic DNA, chromosome complete sequence.
 161586 bp DNA linear FF: 14-July. Homo sapiens chromosome 11, clone KP11-142C4, complete sequence AC090309
 (E-mail:hattoriègsc.riken.go.jp, UKL:http://hyp.gsc.riken.go.jj/.Tel:81-45-503-9111, Fax:81-45-503-9170)
On Dec 7, 2001 this sequence version replaced gl:9927250.
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 McCartiy, M. Meldrim, J. Meneus, L. Mihova, I., Mlenga, V., Marphy, I. N., lor, J., hyuyen, C., Nicol, K., H., Lot, C., Norman, C.H., J., Connor, T., J., Connor, T., J., Chell, D., Oliver, J., Peterson, K., Plankhany, P. Pierre, M., Raymond, C., Retta, K., Rise, C., Rogov, P., Koman, J., Roy, A., Schauer, S., Schupback, K., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, M., Stojanovic, H., Talamas, J., Jesfaye, S., Theodore, J., Topham, K., Travers, M., Vassilev, H., Liner, A., and Zody, M., Wyman, D., Young, G., Zainoun, J., Viel, K., Vo, E., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Viel, K., J., Linner, A., and Zody, M.
 Birren, B., H., Sbaum, C., Lander, E., Ali, A., Allen, H., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhyalter, B., Camarata, J., Charga, T., Chararo, B., Choepel, Y. Colymore, A., Cook, A., Cook, P., Deatellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreita, P., FitzGerald, M., Gage, D., Galagan, J., Garuyna, S., U.J.S., Graham, L., Grand-Pierre, H., Hagos, B., Horto, L., Hame, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Lindblad, D., Major, J., Matthews, C., MacChan, C., Ma
 Johessel, Herlord A., Horton, L., Hulme, W., Illey, I., Johnson, Johnson, Karatas, A., Lañocque, K., Lamazares, R., Landers, T., Lenocky, J., Levine, K., Liu, G., MacLean, C., Mandros Mandro
 Direct Submission
Submitted (17-FEB-2001) Whitchead Institute/MIT Center for Genome
Research, 32 Charles Street, Cambridge, MA 02141, USA
 kesearch, 325 Charles Street, Cambridge, MA 02141, USA
on Aug 1, 2001 this sequence version replaced gi:14595d64.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
 Direct Submission
Submitted (14-JUL-2002) Whitehead Institute/MIT Center for Genome
Jasaarch, 325 Charles Street, Cambridge, MA 02141, USA
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
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 Center code: WIBR
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 linear
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364 46270

Gaps

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PAT 14-JUN-20-2

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REFERENCE
AUTHORS
TITLE
 FEATURES
 COMMENT
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 BASE COUNT
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72; Conserv
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterrield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guif, Letticia Hisiao, Martin Krzywinski, Reta Kutsche, Cliver Lee, Sco Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Mess, Pawan Pandoh, Anna-Litas Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://inage.llnl.gov Series: IRAL Plate: 23 Row: j Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency OKF analysis, Similarity but not identity to protein.
 cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
 Submitted (25-MAY-2001) National Institutes of Health, P
Gene Collection (MGC), Cancer Genomics Office, National
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 200
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrara; Euteleostumi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 BC008353 1646 bp mRNA linear Homo sapiens, Similar to RIKEN cDNA 0610008P16 gene, MGC:15937 IMAGE:3537224, mRNA, complete cds.
 Direct Submission
 Strausberg, R
 BC008353.1 GI:14249941
 info@bcgsc.bc.ca
 (bases 1 to 1646)
 472 a
 Conservative
 TETANS LATION - "MILLINSHKLLALYKSLARS I PESLKYYGSVYH I HEGNEF HHEV LVDSWPEYONVI I PROKOEMTODIDDSYTNYYKHESKEPOKSEEVILKIGE I VIKKGRLG I OGLOESLGEO I RVARTSKSVKVEHSRALLLVTED I I.K.I.NASSKSKLGSKAETIGHEGD EFESETPNYKY AQLOYSYSGLV NDNNARGKNERSLHY I KRC I EDL PAACHLGPENYV SWYTMDPSC EVGHAYSHEKYRTGNHARVHVRYHKYLKOKHI PEY I SVLEEHED SREF VGOTGFFEASCEWHOWTCYPONLVPF SWYTMDPSC EVGHAYSHEKYRTGNHARVHVRYHKYLKOKHI PEY I SVLEEHED SREF VGOTGFFEASCEWHOWTCYPONLVPF SWYTMDPSC EVGHAYSHEKYRTGNHARVHVRYHKYLKOKHI PEY I SVLEEHED SREF VGOTGFFEASCEWHOWTCYPONLVPF SWYTMDPSC EVGHAYSHEY PROKUMARVHVRYHKYLKOKHI PEY I SVLEEHED SREF VGOTGFFEASCEWHOWTCYPONLVPF SWYTMDPSC EVGHAYSHOW PROKUMARVHVRYHKYLKOKHI PEY I SVLEEHED SREF VGOTGFFEASCEWHOWTCYPONLVPF SWYTMDPSC EVGHAY PROKUMARVHYRYHKYLKOKHI PEY I SVLEEHED SREF VGOTGFFEASCEWHOWTCYPONLVPF SWYTMDPSC EVGHAY PROKUMARVHYRYHKYLKOKHI PEY I SVLEEHED SREF SWYTMDPSC EVGHAY PROKUMARVHYRYH PROKUMARVHYRYHKYLKOKHI PEY I SVLEEHED SWYTMDPSC EVGHAY PROKUMARVHYRYHKY PROKUMARVHYRYH PROKUMARVHYR PROKUMARVHYRYH PROKUMARVHYR PROKUMARVHYR PROKUMARVHYR PROKUMARVHYR PROKUMARVHYR P
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/db_xref="taxon:9606"
/clone="MGC:15937 IMAGE:
/tissue_type="Lung, small cell carcinoma"
 Location/Qualifiers
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/db_xref="GI:21438734"
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 Score 43; DB 6; Pred. No. 0.093; 0; Mismatches
 IMAGE: 3537224"
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 283 LIGAAUTGCIACATAAGAIGCTTGIGCTTCATAACTCTCAGAAGCIGCAGATTCIGIATA 342
 343 AATCCTTAGAAAAGAGCATCCCCTGAATCCATAAANGTATATNGC 387
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 VGQFGFEASCEWHQWTCYPQNLVPF*
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 SWVIMDPSCEVGMAYSMEKYRRTGNMARVMVRYMKYLKQKNIPFYISVLEENEDSRRF
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Search completed: Job time : 2896 s

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Post-processing: Minimum Match 0%
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 Sequence:
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| tch Length DB ID | Description        |   |
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| 1189 21          | Human prostate Can |   |
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| Genomic sequence # | AAS28533  | N          | 2405      | a: .2    | ••                | Ļ.<br>Ui     |    |
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| Human immune/haema | AAK73     | N          | 4.1       | ·        |                   | <u>.</u>     | n  |
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| Human immune/haema | AAK70     | w          | 733       |          | 10                | 4-           | c  |
| DNA encoding novel | AAS8483   | IJ         | 4775      |          | , k.              | 4-           | a  |
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| Rat liver toxicolo | Ann       | ю          | 5,,7      |          | ١.                | 36           |    |
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| Human genomic DNA  | AAS32856  | (J)        | 5775      | a.       | υ·<br>t·<br>α     | ÇN<br>ÇN     |    |
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| Human nervous syst | ABAI      | 12         | 9 tu 6    |          |                   | رة.<br>(1)   | o  |
| Human immune/haema | コンスの      | 10         | 5179      |          |                   | α            |    |
| Human nervous syst | ABAI      | 101<br>101 | 5179      |          | ζ,                | 27           | c, |
| Arabidopsis thalia | ABNS      | k)         | 1622      |          | ŀ                 | (%)<br>[2]   |    |
| Human transferase  | HAR       | K.         | 1165      |          | ٠,                | 25           |    |
|                    | AAZ-      | 12         | 1030      |          | ٠.                | to<br>4-     |    |
| Human secreted pro | AACU      | ۲.         | 505       |          |                   | EC.          |    |
|                    | AASE      | į.         | ù         |          |                   | N<br>N       | c. |
| Nucleic acid seque | AAX03468  | 22         | 1635      | מי       | 4.0               | 21           |    |
| Human in PI gene.  | AAX180U2  | N<br>C     | 1035      | ă.5      |                   | 2ċ           |    |
| Rat HRF1 cDNA. Ra  | AA173338  | 1 8        | 1654      |          | <del>-</del> -    | <u>بر</u>    |    |
| 93                 | ABV43691  | ر.<br>درا  | L.        | C        | 4.                | α·           |    |
| Human prostate exp | 1.1       | Ę,         | w         | . · ·    | _                 | 17           |    |
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| Human prostate exp | -         | ١,         | u         | ,<br>C   | <u>ئ</u><br>د . د | ĽΠ           |    |
| ostate             | 1. 1      | I.         | a<br>a    | <u>.</u> | <u>.</u><br>ن     | •—1<br>•4    |    |
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## **ALIGNMENTS**

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Dieast cancer; therap; Mamood: 88.
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 Haman breast specific gene crope Mamd04
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ting, ulaymosing, monitoring, staging, prognosticating, imaging reating breast cancer using protein product of breast specific
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 invention relates to methods for diagnosing, monitoring, stails, mainter and treating breast cancer (BC). The methods comprise measured, the levels of BSC products in cells, tissues or body fluids of the patient and comparing the measured levels of BSC, with BSC levels of a formal human control. An antibody against the BSC sequences can be adelicable used for imaging BC in a patient, the antibody seam be computed in a cytocoxic agent, and used for treating BC in a patient.
 Claim 6;
 AAH76198
 16-AUG-2001
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 29-0C1-2001
 Sequence
 sequences
 hepatotrophic;
 361
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 241
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 181
 181
 121
 121
 61
 61

 sequence represents a breast specific gene (650) clone. The 653 ences are also referred to as breast specific markers (65M). How
 metabolizing enzyme; DME; immunosuppressive;
totrophic; antiallergic; antiasthmatic; antiba
 ICCCCTGAATCCATAAANGTATAINGCG 388
 TUTCTATGGACAGAACGTCTGGTTTAATCTACAGGAACCCATAACTTCCTGAAGCTTTAT :::
 388; Conserv
 drug metabolizing enzyme encoding cDNA (ID No.
 Page
 388
 therapy; gene
 99.5%: Score 386; DB 21; ilarity 100.0%; Pred. No. 6.6e-110; Conservative 0; Mismatches 0;
 БP;
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 39; 45pp; English.
 Location/Qualifiers
391..1275
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 115 A; 83 C; 77 G; 111 T; 2 other;
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 antiasthmatic; antibacterial;
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 The invention formions homon drug metabolizing enzymes (DME) and polymoslections encoding the IMES. The IME can be expressed by standard recombinant northodology. FMES and their agonists and antagonists are useful for the diagnosis, treatment, and prevention of autoimmune/ inflammatory cell proliferative, developmental, endocrine such as an entrysa, the metabolic, and gastrointestinal disorders, including liver disorders and infection. The present sequence represents a human EME
 Isolated foly optime encoding a drug metabolizing enzyme useral diagnosis, the ament, and prevention of autoimmune/inflammatory, prollibrative developmental and endocrine disorders.
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 neuroprotective; cytostatic; cardioactive; immunomodulator; husecons; vulnerary; gastrointestinal; nephrotropic; antiinfective; grasecol; antibacterial; gene therap; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
 nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
 Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer -
 AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AA557302 The prostate cancer antigens can have neuroprotective, cytostatic cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal cardioactive, g
 Claim 1;
 (HUMA-) HUMAN GENOME (ROSE/) ROSEN C A.
 12-MAR-1599;
 08-MAR-2000; 2000WO-US05988
 21-SEP-2000
 Human
 Sequence 1189 BP; 333 A; 245 C; 300 G;
 16-SEP-2002
 ABV24501 standard; cDNA; 1390
 363
 343
 2000-587513/55
 AATCCTTAGAAAAGAGCATCCCCTGAATCCATAAAANGTATATNGC 367
 AATCCTTGGCCAGGAGCAT-CCCTGAGTCCCTGAAGGTGTATGGC
 prostate
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 Page 693-694; 2338pp; English.
 Conservative
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 cancer antigen nucleotide sequence SEQ ID No.125
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RESULT 5
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 s nucle that sequence given in Tables 1-9 (ABV00010-ABV62213) of the specific which are its complement. (I) is useful for:

(a) assesting whether a partient is affiliated with prostate cancer:

(b) mother thing the progression of prostate cancer in a patient:

(c) assesting the efficacy of a test compound to inhibit prostate
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-ing the efficacy of a therapy for inhibiting prostate cancer
 -o useful as a pharmacodyanamic or pharmacogenomic marker.
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while and correlating with presence of prostate cancer, useful
that presence of prostate cancer, stage of prostate cancer.
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 ion relates to an isolated nucleic acid molecule (I) comprising de sequence given in Tables 1-9 (ABV00010-ABV62213) of the
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2 2008-207454P.
2 20008-211314P.
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 Carcinogen; pharmacodyanamic marker;
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 The invention relates to an isolated nucleic acid molecule (i) connectsing a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer:

(b) monitoring the progression of prostate cancer in a patient:

(c) assessing the efficacy of a test compound to inhibit prostate
 Human prostate expression marker cDNA 24706
 Séquence
 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, userul for detecting presence of prostate cancer, stage of prostate cancer.
 ABV24715 standard;
 concer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer

 (e) selecting a composition for inhibiting prostate cancer in a patient;
 (f) assessing the prostate cell carcinogenic potential of a compound;
 (g) determining whether prostate cancer has metastasized in a patient;
 (h) assessing the aggressiveness or indolence of prostate cancer in a

 Claim 1; Page 4654; 11750pp; English.
 WPI; 2001-662795/76
 18-JUL-2000;
 16-MAR-2000;
25-MAY-2000;
 pharmacogenomic
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 17-FEB-2000;
 20-FEB-2001;
 WO200160860-A2
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 283 CIGAAGTGCTACATAAGATGCTTGTGCTTCATAACTCTCAGAAGCTGCAGATCTGTGTATA 342
 AATCCTTAGAAAAGAGCATCCCCTGAATCCATAAANG1AIAINGC
 CTGAAGCATCCCACAGAATGATCCTACTGAATAACTCCCATAAGCTGCTGCGCCTATACA
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(c) assessing the efficacy of a test compound to inhibit prostate
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 Sequence lime by 384 A; 328 C;
 First isolated nucleic acid molecule associated with cancerous state prostate cerls and correlating with presence of prostate cancer, usen for detecting presence of prostate cancer, stage of prostate cancer.
 . 09-1308-2000: 2000US-211314P.
16-30E-2600: 2-00US-215007P.
1--15-2000: 2-000US-255281P.
 Ciam 1: Faue 4713; 11750pp: English.
 Silling fel K.
 1c-MAR-2000;
25-MAY-2000;
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 20) OTGAA HAGCTACATAAAA KOTTGTGGTTGTAAACTCTCAGAAGCTGCGGAGATTGTGTATA 342 HTHH | HTHHH | HTHHHH | HTHHHHH | HTHHHHHH | HTHHHHHAGA 421
 40-833-2001.
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 selecting a composition for inhibiting prostate cancer in a patien assessing the prostate call carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient assessing the aggressiveness or indolence of prostate cancer in a
 assessing the efficacy of a therapy for inhibiting prostate cancer
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 'er in a patient;
 ALL-POITSGCAGGAGCAL-CCCTGAGTCCCTGAAGGTGTATGGC
 edl Standard; chila;
 AATOTI TAGAAAAGAGCA LOCCUT JAATGCATAAANG TATATNGO
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 2001-6-27 15/76
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 Similarity
 MILLENGIUM PREDICTIVE MEDICINE
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 2000US-207454P
 ZJUUUS-idssiyP
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 expression marker chia
 market; gene:
 cancer: cytostatic;
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 Saute 43;
 Pred. No.
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 carcinogen;
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 0.0042;
 321 T; 7 other;
 INC
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 pharmacodyanamic
 Indels
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RESULT 8
ABV27695
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XX ABV2
XX ABV2
XX ABV2
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 Matches
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 09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
 The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1.9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
 WPI;
 Human; prostate pharmacogenomic
 ABV27695 standard;
 Sequence 1390

 (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a partient;
 (e) selecting a composition for inhibiting prostate cancer in a partient;
 (f) assessing the prostate cell carcinogenic potential of a compound;

 Claim 1; Page 5013; 11750pp; English.
 Novel isolated nucleic acid molecule associated with cancerous prostate cells and correlating with presence of prostate cancer
 16-MAR-2000;
25-MAY-2000;
 20-FEB-2001;
 WO200160860-A2
 Homo
 ABV27695
 cancer in a patient;
 (MILL-)
 16-SEP-2002
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44
اوا
 362
 Local
 selecting a composition for inhibiting prostate cancer in a patient assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
 detecting
 CIGAAGTGCTACATAAGATGCTTGTGCTTCATAACTCTCAGAAGCTGCAGAAITCIGIATA 342
 sapiens
 AATCCTTGGCCAGGAGCAT-CCCTGAGTCCCTGAAGGTGTATGGC
 AATCCTTAGAAAAGAGCATCCCCTGAATCCATAAANGTATAINGC
 CTUAAGCATCCCACAGAATGATCCTACTGAATAACTCCCATAAGCTGCTGUUUCTATACA 421
 2001-662795/76
 prostate
 also
 MILLENNIUM PREDICTIVE MEDICINE
 similarity
 cells and correlating with presence of prostate cancer, cting presence of prostate cancer, stage of prostate cancer.
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 ; 2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
 Conservative
 useful
 2001WO-US05171
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 Endege WO,
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 expression marker cDNA 27686
 marker;
 cancer;
 364 A; 328 C; 350 G;
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 CDNA; 1390
 entry)
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 gene; ss.
 cytostatic;
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 Monahan JE;
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 Pred. No.
 Score 43;
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 carcinogen;
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 321 I; 7 other;
 DB 23; Length 1350;
 or pharmacogenomic
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 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleutive sequence given in lables 1.9 (ABV00010-ABV62213) of the
 Human; antiangemic; subperary; antiinflammatory; immunomodulator; antiinfertilit;; cerebroprotective; cytostatic; rheumatic; gene treuroprotective; antiparkinsonian; protein therapy; EST;
 cancer in a justient:
 specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer:
(b) monitoring the progression of prostate cancer in a patient;
 Claim 1; Page
 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
 09-JUN-2000;
18-JUL-2000;
 NOTEL Limit Colling Sequence
 9
 (e) selecting a composition for inhibiting prostate cancer in a patien(f) assessing the prostate cell carcinogenic potential of a compound;(g) determining whether prostate cancer has metastasized in a patient;
 WPI: 2001-602795/76
 16 -MAR - 2000;
25 -MAY - 2000;
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 expressed sequence tag:
 in a patient:
 ABN5v651
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 JELA TORAGON: "COACAGAATGATCOTRATAGATAGCTCCCATAAGCTGCTGGCCCTATACA 421
 283 CIGABGI FIACATAAGAIGCIIGIGETTCATAACICTCAGAAGCTGCAGATTCIGTATA 542
 monitorily the progression of prostate cancer in a patient; dassessing the efficacy of a test compound to inhibit prostate
 detecting presence of prostate cancer, stage of prostate cancer
 is also
 assessing the aggressiveness or indolence of
 sapiens
 1 Similarity
72: Caser
 MILLERHIUM PREDICTIVE MEDICINE
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 stantard;
 12 COOUS-18986LP
12 COOUS-2:7454P
12 COOUS-211314P
12 COOUS-219007P
12 COOOUS-255261P
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 .setul as a pharmacodyanamic or pharmacogenomic marker.
 Elidede Wa
 5679; 11750pp; English.
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 J1W0-08J5171
 384 A; 328
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Pred. No.
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 rheumatic; gene therapy;
apy; EST;
 Length 1390;
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 a patient;
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RESULT 10
AAH23819
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 Matches
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 The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESIS) They can be used to stimulate cell growth, to reallate e.g. to treat aplastic anaemia, to help tissue reduction multiple sclerosis, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibit e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatorid arthritis, and to treat nervous system disciders e.g. parkingon's disease. The present sequence is a coding sequence of the
 21-MAK-2002
 An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis \dot{\gamma}
 Xue
 11-SEP-2000; 2000US-0659671
 atherosclerosis; hepatitis; psoriasis; cancer; tumbur; inflammation; AIDS; Addison's disease; allergy; astimus; stream; cirrhosis; Crohn's disease; atopic dermatitis; disabetes merities; multiple sclerosis; rheumatoid arthritis; pancreatitis; systemic lupus erythematosus; thrombocytopenia; ulcerative colitis; haemodialysis; extracorporeal circulation; trauma; transgenic anima
 Claim
 (HYSE-)
 10-SEP-2001; 2001WO-US26015
 CDS
 Homo
 yene
 Human transferase: HTFS; agonist; antagonist; cellular stabilities proliferation; cell proliferative disorder; immune disorder:
 31-JUL-2001
 AAH23819
 AAH23819 standard; cDNA; 1955 BP
 sequence 1627
 Human
 370
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 310
 283
 Local Similarity
 CIGAAGIGCTACATAAGATGCTIGTGCTTCATAACTCIGAGAAGCIGCAGAITGIGIAIA 342
 2002-292408/33
DB; ABE97238.
 AATCCTTGGCCAGGAGCAT-CCCTGAGTCCCTGAAGGTGTATGGC
 AATCCTTAGAAAAGAGCATCCCCTGAATCCATAAANGTALATNGC
 sapiens
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 BP; 472 A; 336 C; 394 G; 420 I; 5 other;
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 Location/Qualifiers 270..1178
/product= "HTFS-19"
/function= "Transferase"
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 Wehrman
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 HTFS-19 CDNA, SEQ ID NO:61
 screening;
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Matches 7
 remains to the compositions comprising an HITS protein. HITS appoints the protein of security of security and seed to condition associated with use issue of increased expression of functional HITS. Disorders which use issue of increased expression of functional HITS. Disorders which is use treated using such compositions include cell proliferative disorders. For example, diseases which may be treated. Those atheroscierosis, hepatitis, paoriasis, cancers (including treater) bone marrow, brain and uterus cancer), inflammation, AIDS. Autocomb disease, allergies, asthma, anaemia, cirrhosis, Crohn's disease, topli dermatitis, dishetes mellitus, multiple sclerosis, the matter attricts, pancreatitis, systemic lupus erythemacosus, thombol, uponia, and ulcerative colitis. They may also be used to treat cround it is hackatopoletic cancer, including lumphome lankacemition.
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 AABT3494-AABT3535 represent novel human transferase proteins Bits-42, and septembes AAB23801-AAB23842 represent cDNAs nem. The proteins play important roles in the regulation of hypatiling and proliferation. The HTFS proteins are useful for compounds for their effectiveness a agonists or antagonists or activity, or for compounds that specifically bind to an HTFS exacts modulates the activity of an HTFS protein.
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RESULT 12
ABV23508
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 16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
 The invention gelates to an isolated nucleic acid molecule (1) com a nucleotide sequence given in Tables 1-y (ABV00010-ABV62213) of the specification or its complement (1) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
 ABV22908
 ABV22908 standard;
 Sequence 358
 Claim
 20-FEB-2001; 2001WO-US05171
 23 - AUG - 2001
 WO200160860-A2
 pharmacogenomic
 ABV42132
 17-FEB-2000;
 16-SEP-2002
 182
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 Local
 assessing the efficacy of a therapy for inhibiting prostate cancer
 selecting a composition for inhibiting prostate cancer in a pattern assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
 el isolated nucleic acid molecule associated with cancerous state state cells and correlating with presence of prostate cancer, used detecting presence of prostate cancer.
 AATCCTTGGCCAGGAGTAT-CCCTGAGTCCCTGAAGGTGTATGGC
 CTGAAGIGCTACATAAGATGCTTGTGCTTCATAACICICAGAAGCIGCAGATICIGIATA 342
 AATCCIIAGAAAAGAGCATCCCCTGAATCCATAAANGTATATAINGC
 1;
 prostate
 also
 Similarity
 MILLENNIUM PREDICTIVE MEDICINE INC
 ₩,
 Page 8445; 11750pp; English.
 2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
 useful as
 Conservative
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 expression marker cDNA 42123
 marker; gene; ss
 cancer; cytostatic;
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 CDNA;
 NO.
 A; 85 C; 52 G; 87 T; 0 other:
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 Score 41.4; Db 23,
Pred. No. 0.0077;
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 The invention is saled to an isolated nucleic acid molecule (1) comprising a nucleotide select given in Tubles 1-9 (Abv00010-Abv62213) of the specification of its complement. (1) is useful for:

(a) assessing a cher a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
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08 - 107454P

08 - 211314P

08 - 21502P

08 - 255281P
 The Carle molecule associated with cancerous state of
it currelating with presence of prostate cancer, useful
source of prostate cancer, stage of prostate cancer -
 -apposition for inhibiting prostate cancer in a patient;
prostate cell carcinogenic potential of a compound;
netter prostate vancer has metastasized in a patient;
againssiveness or indolence of prostate cancer in a
 , etticacy of a therapy for inhibiting prostate cancer
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 121.3AGGGAAAGAAG--CIGAAGIGCTACATAASAIGCITGIGCIIC
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Matches 74
 16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-215007P.
13-DEC-2000; 2000US-255281P.
 Human prostate
 Sequence 388 BP; 94 A; 77 C;
 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
 16-SEP-2002
 ABV28712 standard;
 Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, used for detecting presence of prostate cancer, staye of prostate cancer.

(e) selecting a composition for inhibiting prostate cancer in a patient
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

 Claim
 Human
 patient;
 Schlegel R,
 (MILL-) MILLENNIUM PREDICTIVE MEDICINE
 17-FEB-2000;
 20-FEB-2001;
 E0200160860-A2
 pharmacogenomic
 (d) assessing the
 153
 313
 93
 Local Similarity
 a patient;
 ATAACTCTCAGAAGCTGCAGATICTGTATAAATCGITAGAAAAGAGCATCGG 354
 TTCAGATCATCTTGAGGGAAAGAAG--CTGAAGTGCTAGATAAGATGCTTGTGCTTC
 ATAACTCCCATAAGTTGCTGGCCCTATACAAATCCIIGGCCAGGAGCATCCC
 TTCAGAGTTTCTTCATCAAGGTCTCAAGGTCTGAAGCATCCCACAGAATGATCCTACTJA
 prostate expression marker cDNA 22903
 also
 prostate
 Page 4060; 11750pp; English.
 useful as a pharmacodyanamic or pharmacogenomic marker
 patient;
 Conservative
 Endege WO,
 2000US-183319P
2000US-189862P
 2001WU-USU5171
expression marker cDNA 28733
 marker;
 efficacy of a therapy for inhibiting prostate cancer
 cDNA;
 10.48;
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 gene;
 cytostatic; carcinogen; pharmacodysmanic marker;
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 Score 40.4; DB Pred. No. 0.016;
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RESULT 15
ABV13728
ID ABV13
 Guery Match
Best Local Similarity
Matches 74; Conserv
 cancer in a patient:
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
 The invention relates to an isolated nucleic acid molecule (1) comprising a nicreotide sequence given in Tables 1-9 (ABV00010-ABV62213) or the specification or its complement. (1) is seeful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the utilizacy of a test compound to inhibit prostate
 Moved isolated to lettracia molecule associated with eaccerous state of prostate cancer, useful prostate cancer.
Hullan prostate expression marker
 sequence sam
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 ABV13728 Stabiard:
 Claim 1; Page 6037; :1750pp; English.

 is also useful us a pharmacodyanamic or pharmacogenomic marker.

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 255 TICAGATCATCITUTT TAGUGAAAGAAG--CTGAAGTGCTACATAAGATGCTTGTGTTTC
 2-1-868-20 11
 20-203-200
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 assessing the prestate cell carcinogenic determining whether prostate cancer has massessing the aggressiveness or indolence
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 Pharmacodyanamic marker;
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Search completed: January
Job time : 232 secs
 Matches
 Query Match 10.4%;
Best Local Similarity 66.1%;
 17-FEB-2000; 2000US-183319P.
16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
 (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound: (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
 The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62313) of the specification or its complement. (1) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
 Novel isolated nucleic acid molecule associated with cancerous state oppostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
 pharmacogenomic
 Claim 1; Page 2279; 11750pp; English.
 WPI; 2001-662795/76.
 schlegel R,
 23-AUG-2001.
 KU200160860-A2
 Homo sapiens
 20-FEB-2001; 2001WO-US05171.
 Sequence 392 BP; 96 A; 77 C; 102 G; 114 T; 3 other;
 cancer in a patient;
 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC

 is also useful as a pharmacodyanamic or pharmacogenomic marker.

 255 TTCAGATCATCTTCTTGAGGGAAAGAAG---CTGAAGTGCTACATAAGATGCTTGTGCTTC 512
 313
 157
 97
 TTCAGAGTTTCTTCAAGGTCTCAAGGTCTGAAGCATCCCACAGAATGATCCTACTGA 156
 74;
 Conservative
 Endege WO,
 marker;
 'n
 gene;
 Monahan JE;
 2003, 13:48:57
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 Score 40.4; DB 23; Length 392; Pred. No. 0.016;
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Perfect score:
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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 scoring table:
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 Database :
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Listing first 45 summaries
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138.8
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1: em_
2: em,
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388
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3224.140 Million cell updates/sec
 Query
Match
 16154066 seqs, 8097743376 residues
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Tissue Procurement: AICC

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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 mRNA sequence.
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 (pieteridejony.med.burfalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm.) or from Resear h Genetics (infoiresyen.com). bAC end Web Server:
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Class: BAC ends
 http://www.htsc.washington.edu
Plate: 1152 row: I column: 10
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 /note-"Yector: pBACe3.6: Site_1: EcoRI; Site_2: EcoRI: Maie blood DNA was isolated from one randoml; chosen is and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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 http://image.llnl.gov
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 602502206F1 Nim_M3C_75 Homo sapiens cDNA clone IMAGE:4615825
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Tissue Procurement: CLONTECH Laboratories, Inc.
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Contact: Robert Strausberg, Ph.D.
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 TCCTTGGCCAGGAGCAI-CCCTGAGTCCCTGAAGGTGTATGGC
 FCCTTAGAAAAGAGCATCCCCTGAAFCCATAAANGTATATNGC 387
 The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD
Tel: 3018699056
 Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloped human infant brain cDNA library
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleust.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 376)
 Homo sapiens
 AA340632
AA340632.1 GI:1592945
EST.
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EST45962 Fetal kidney I Homo
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 Contact: Kerlavage, AR
 Other_ESTs: THC95311
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 For clone availability, additional sequence and expression information related to this ESI, please check the IIGK Hum. Index (http://www.tigr.org/tdb/hgi/hgi.html)
 Bioinformatics
 Email: arkerlav@tigr.org
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 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nlh.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiAL)
 Email: cgapbs-remail.nih.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostimi;
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Contact: Robert Strausberg, Ph.D.
Email: cgupbs-ramail.nih.yov
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Mammalia; Eutheria; Primetes; Catarrhini; Hominidae; Homo.
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Contact: Robert Strausberg, Ph.D.
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DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution injurnation can be
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Contact: Robert Strausberg, Ph.D.
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
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DNA Sequencing by: Incyte Genomics, Inc.
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Sequence 52. Application 08/08037500 Patent N. 5932442 : GENERAL INFORMATION:

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| DB 4; 44; 38; GCIICAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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; CLONE: 208836
US-Vē-933-750C-62
 Query Match 8.0%;
Best Local Similarity 57.3%;
Matches 55; Conservative
 Sequence 62,
 Patent No.
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 APPLICANT:
APPLICANT:
APPLICANT:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 1182 CCATTACTTAGGTTTCCCCATAATTCTIAAATTTAAA 1217
 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
 APPLICATION NUMBER: U
FILING DATE: Septembe
CLASSIFICATION: 536
PRIGR APPLICATION DATA:
 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DAFA:
 NUMBER OF SEQUENCES: 98
 APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TIILE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
 REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: 115-855-0555
 CORRESPONDENCE ADDRESS
 APPLICANT:
 APPLICANT:
 1122 GAGCIACAGGAGAGGGTGGTGCTTCCGACTTGCCAGAAGACCCCGGAIGAGGATGCAAIIC 115
 SEQUENCE CHARACTERISTICS:
 APPLICANI: Yue, Henry
APPLICANI: Guegler, Karl J.
APPLICANI: Corley, Neil C.
TITLE OF INVENTION: HUMAN R
 288 GIGCIACATAAGATGCTTGTGCTTCATAACTCTCAGAAGCTGCAGAITCIGIAIAAACCC 347
 348 TTAGAAAAGAGCATCCCCTGAATCCATAAANGTATA 383
 APPLICATION NUMBER: FILING DATE:
 COMPUTER: IBM CONTROL OPERATING SYSTEM:
 STREET: 3174 POI
CITY: Palo Alto
STATE: CA
 TOPOLOGY:
 STRANDEDNESS:
 TELEFAX: 415-845-4166
 COUNTRY:
 LENGTH:
 94304
 nucleic acid
 Application US/09234613
 1249 base pairs
 USA
 Au-Young, Janice
Yue, Henry
 Hillman, Jenniter I..
Bandman, Olga
 SPLNNOT 02
 Shah, Purv
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 IBM Compatible
Incyte Pharmaceuticals, Inc
 September 23, 1997
N: 536
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 US/08/935,750C
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 Score 31; DB 2; Length 12; Pred. NO. 2; 0; Mismatches 41; Indels
 PF-0356
 DB 2: Length 1249:
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: NAME/KEY: (7DS); (1777); (15)-(1777); (15)-(1777)
 US-09-234-615-62
 Sequence 1 Application US/valays77
Facent No. 6045321
GENERAL INFORMATION:
 SEQ ID NO 1
LENGTH: 1802
 Hest Local Similarity 57.3%;
Matches 55; Conservative
Best Local Similarity
 CURRENT APPELICATION NUMBER: US/09/289,377
CURRENT FILING DATE: 1999-04-09
NUMBER OF SEG (D. NOS: 47
 TITLE OF INVENITOR: ANTISERSE MODULATION OF G-ALPHA-II EXPRESSION FILE REFERENCE: RIS-0056
 APPLICALI
 INFORMATION FOR SE, ID N & SEQUENCE CHARACIERISTICS:
LENGTH: 1245 Lase Lair
 19-209-377-1/0
 TYPE: DNA
DRGANISM: Homo sapiens
FEATURE:
 CLMPUTER REALABLE FORM:
MEDION TYPE: THIS MEATURE
COMPOTERS IBM COMPACTION
OPERATING SYSTEM: D.S
SOFTWARE: FASTSED TO HIDOMA Version
OURRENT APPLIATION DATA
APPLITATION WOMBER: US/03/244-013
 1122 GAGGIACAGGAGGGGGGGGGACAGAGACCCCGAGGAGCAGCATIC 11d
 1162 CONTROLLAGITICOUNTANTOTIANATTIANA 1217
 REGISTRAIT A NAMEER: 36,749
REFERENCE/COCKET NUMBER: PFT
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415-855-0555
 APPLICATI R BURBER: 05/A
FILING LATE: September 2
ATTORNET/AGES: HEFORMATION:
 PRICE APPLICATION DATA:
 IMMEDIALE SCURGE:
 266 GIGCIACETAEGATGCTIGIGCTICATAACTCICAGAAGCTGCAGATICIGIATAAA1CC 347
 348 TIAJAAAAJAGTAICOPUIGAATUJALAAAAGTATA 383
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 13431
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 Sequence 677, Appl
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 sequence 677, Application US/09134001C Patent No. 6380370
 Eest Local Similarity
Matches 56; Conserva
 NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 677
 GENERAL INFORMATION:
 Patent No.
 séquence
 APPLICANT: Lynn Doucette-Stamm et al IIILE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING IIILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT EFLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,564
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
 TYPE: DNA
 LENGTH: 1578
 COMPUTER KEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
 SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
 TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE NUMBER OF SEQUENCES: 143
 CLASSIFICATION: 424
PRICK APPLICATION DATA:
 CORRESPONDENCE ADDRESS
 288 GIGCTACATAAGATGCTTCTGCITCATAACTCTCAGAAGCTGCAGAITCTGIAIAAATCC 347
 889 ATCCTGCATATTCTGGATA 671
 829 ITITACAATACCAGAACAAATAACTAATAACAAATATAGC 750
 348 TTAGAAAAGAGCATCCCCTGAATCCATAAANGTATAINGC 387
 CITY: New York
STATE: New York
APPLICATION NUMBER: US 08/075,783 FILING DATE: 11-JUN-1993
 APPLICATION NUMBER: US/08/257,073 FILING DATE: 09-JUN-1994
 COUNTRY:
 STREET:
 ADDRESSEE:
 AAGCTGCAGATTCTGTATA 342
 10, Application US/08257073
5, 5766597
 INFORMATION:
 10036
 New York
 E: Curtis, Morris & Safford, P.C
530 Fifth Avenue, 25th Floor
 Conservative
 UNITED STATES OF
 7.98;
 Release #1.0, Version #1.30
 0; Mismatches 44;
 Score 30.8; DF Pred. No. 2.5;
 DB 4; Length 1570;
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 US-jā-257-
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 KESULT 7
 US-09-453-7
 IELLAN: (212) 840-3333
IELLAN: (212) 840-0712
IELLAN: 425066 CURINS
INFORMALI N FOR SEQ ID NO: 10:
SEGUEN E CHARACTERISTICS:
LEN'IN: 5]ul base pairs
 Query March
Best Luci Similarity F2.4
Matthew of Conservation
 Sequence of Application US/U94537026
Patent 5 (36572)
 PRI F N. 110A. N. DALAN
ALTA N. MSER US 07/852.305
FILL V. DATE: 16-MAR-1992
PRI F N. PLICKI, N. DATA:
ALIA MITON NIMBER: 08-07/672.003
 FEST CHASTICK NUMBER: 25,506
KERT ENCEZO PIKES NUMBER: 45
TEST CHASTICAL IN INFORMATION:
 FILLS DATE: 20-MAR-1991
ALL SELEZAGEN, SKEDEMASI NE
 3535 A A 3 353c
 Ter .-10
 300 2.33 386
 TYPE nucleic acid
STRAN, EDNESS: single
 Art. ICANI: blactness, Frederick
 FEST MUENCE ADDRESS:
 _b-166/7
 KNEY/AGENT INFORMATION:
 R APPLICATION DATA:
 Frommer, William S
 CHY: Madison
STATE: WI
 STREE!:
 SELMOOD
 ADDRESSEE: Qualles a brady
 NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
 SSFINAKE: Word Portect 6.0
 linear
 SEQ ID No: lu:
 Flunkett,
 Burland,
 erna,
 Us.
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 Stare 30.8; DE Fred. No. 4.2; o: Mishatches
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HitteR OF INTENTION: ND. 536572561 Sequences of MitteR OF SEQUENTES: 265
 ZIP: 55701-2115

MEDIUM TYPE: DISKette 3.50 inch. 1.44Mb Storage COMPUTER: IBM PC compatible operating System: pc-1/28/MS-DOS
APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998
 1 Stich Pinckney Street
 E. puli ul57
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 D)
 US- US-453-702B-166
 US-08-518-474-1/c
 Sequence 1, Application US/08518474 Fatent No. 5599920
 Marches
 Eest Local
 GENERAL INFORMATION:
 APPLICANT: Patel, Pragna I.
APPLICANT: Suter, Ueli
APPLICANT: Snipes, G. J.
APPLICANT: Welcher, Andrew
APPLICANT: DeLeon, Marino
APPLICANT: Lupski, James R.
APPLICANT: Shooter, Eric M.
TITLE OF INVENTION: SEQUENCE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 INFORMATION FOR SEQ ID NO: 166: SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: Patentin Release #1.0, Version #1.25
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/08/518,474
FILING DATE: 21-AUG-1995
CIASSITICATION: 126
 CORRESPONDENCE ADDRESS
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,488
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 07/879,623
 FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
 NUMBER OF SEQUENCES:
 TELECOMMUNICATION INFORMATION:
 860 CITGATCAACAGCAAGCTAATGATGTCCTTGCTGTTTTACAAAGACA 6.4
 207 ACTGAGAAACTGGCAGCAGGCAGGCCTACAGGTCTACAAAGAAA 253
 7.8%;
Local Similarity 55.1%;
hes 59; Conservation
 TELEFAX:
 COUNTRY: USA
ZIP: 77010-3095
 CIIY: Houston
STAIE: Texas
 TELEPHONE: 713/01.
 REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
 STREET:
 CLASSIFICATION:
 NAME:
 ADDRESSEE:
 REFERENCE/DOCKET NUMBER: 960257,95017
IELECOMMUNICATION INFORMATION:
IELEPHONE: (608) 251-5000
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 166:
 Paul, Thomas D.
 TYPE: nucleic acid
STRANDEDNESS: double
 LENGTH: 16950
 762829
 ELEFAX:
 1301 McKinney, Suite 5100
 Fulbright & Jaworski
 713/651-5151
 (608)
 PERIPHERAL MYELIN PROTEIN COLING SEQUENCE AND METHOD
 32,714
 251-9166
 0; Mismatches 48; Indels
 D-5331-CIP
 Score 30.2;
Pred. No. 11;
 DB 4; Lenyth 16950:
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 : Sequence 52, Application US/upl727.i
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Sequence i. Applitation dS/va72oufd
Patent i.. 587174
GERRAL IMPORMATE A:
APPLICANT: Salth, Claig A:
INTLE OF INVENTION: Chemoking Inhibitor
NUMBER OF SIQUENCES: 7
CORRESPONDENCE ADDRESS:
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 . UHER INFORMATI N: 70060a£61hi
05-09-172-711-5.
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 WALE THE INPER COME
US-ca-51a-174-1
 US-08-72"...50-1
 US-09-172-711-52
 RESULT 10
 : SEQ ID N 52
: LENGTH: 295
: TYPE: DWA
 East Local Sim
 APPLINANT: Canadaman, Mary James
APPLINANT: Exclusi, Gary b.
APPLINANT: Panzer, Scott F.
APPLINANT: Selfhamer, Jettrey J.
TITLE of INVENTIANT MONITORING I ALCOHOGICAL RESPONSES
FILE REFERENCE: PANDOTTOR CONTROLL OF THE
 GENERAL INFORMATION:
 best boral Shalacity 50.76;
Mutches 72; Conservative
 CURKERL APPLICATION HUMBER: US/09/172,711
CURRENT FILING GAIE: 1558-10-13
HUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
 NAME/KEY: unsure
LOCATION: 35
JHER INFORMATION: a or g or P of E. diknown,
FEATURE:
 ORGANISM: Home sapiens
 FEATURE:
 SEZ TRANCASCERSCOCASCIONA SEL
 293 FACATAAGATSCIIGIGCIICAFAACICICAGAAGCIGCAGATICIGTATAAATCCIIAG 351
713 FALATUTAAAAGIGTIATAAAAAAGCITTATAAACCGGAGATATTATATACATCIICAA 683
 232 I SCOTA DE STICTACARAGRAS I I DAGATORIO TOTTORAGOGRARAGRAGOTORAGIOC 291
 115 AAJATATT ATTIGGAAATTCAGAAATGCIGGAGATGTTGGAGATGCTTAAGGAAA 175
 297 AAGATUUTTUUTGOTTOATAADIOTOAGAAGOOTOOAGATTOTGTATAAATOOTTABAAAAG 356
 552 AAAAGAGCA. 2000TGAATCCA 575
 STRANDEDNESS: Single
 n Rott Soute 29.6;
Similarity 64.4%; Fred. No. 2
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RESULT 11
US-08-381-691-17
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 US-08-720-258-1
 Sequence 17, Application US/08381691
Patent No. 5852224
 Query Match
Best Local Similarity
Matches 51; Conserv
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,715
FILING DATE: 20-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,324
FILING DATE: 29-SEP-1995
ATTORNEY/AGENT INFORMATION:
 GENERAL INFORMATION:
 SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple System 7.5.3
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
TIFLE OF INVENTION: Alpha-lac Albumin Gene Constructs NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:
 FEATURE:
 FEATURE:
 IMMEDIATE SOURCE:
 ANTI-SENSE:
 HYPOTHETICAL:
 MOLECULE TYPE:
 276 AAAGAAGCTGAAGTGCTACATAAGATG 302
 TELEPHONE: (20b) 307 CT.
TELEFAX: (206) 233-0644
TELEX: 756822
TELEX: 756822
 108 ACGGAAGAAGAAACAACATCATATG 134
 NAME/KEY:
LOCATION:
 APPLICATION NUMBER: US/08 FILING DATE: 26-SEPT-1996 CLASSIFICATION: 435
 NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2620-8
 COUNTRY:
 NAME/KEY: mat_peptide LOCATION: 66..755
 LOCATION:
 NAME/KEY:
 CLONE: Cowpox p35
 STRANDEDNESS:
 LENGTH: 758 base pairs
 ADDRESSEE:
 98101
 Seattle
 nucleic acid
 Washington
 E: Immunex Corporation
51 University Street
 Conservative
 CDS
18..758
 sig_peptide
18..65
 N
O
 linear
 NO
 CDNA
 single
 7.6%;
58.6%;
 US/08/720,258
 0; Mismatches
 Score 29.4; bb 2; Length "5b; Pred. No. 5.1;
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RESULI 12
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 US-08-381-691-17
 : ORGANISM: numu sepiens
US-v9-357-206-4
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best Tocal substarity
Matches 54: Conserv
 NUMBER OF Shy ID NOS:
Shy ID NO 4
LENGTH: 2:71
TYPE: DNA
 GENERAL INFURMATION:
 Sequence 4. Application US/09367206 Patent No. 6326482
 Matches
 PRIS N APPLI MITCH NUMBER: PCI/US99/0884
PRIS N FILLI (AE: 1999-04-23
PRIS RILLI (AE: 1999-04-23
PRIS RILLI (AE: 1996-04-23
PRIS FILLI (AEE: 1996-04-23
PRIS APPLI AIGH NUMBER: US 60/113,296
PRIS APPLI AIGH NUMBER: 1596-12-22
NUMBER OF SEG-10 N.S: 55
 APPLICANT: Generatech, In
TITLE OF INVENTION: MSP
FILE REFERENCE: P1223KIE
 est local Similarity
 CURRENT APRICATION NUMBER: US/09/367,206
 APPLICATION NUMBER: US.
INF. FMATION FOR SEV ID NO.
SECUENCE CHARACTERISTICS:
 ANTI-SENSE: NO
 PERATING SYSTEM: (12-Foc/MS/105)
SUBJUMENT: Patenthic metersor floor, Version #1.30 (EM)
CURRENT APPLICATION DATA:
 1764 AGCLICATOTTIGGGAAAGCHACIGHIHHGAIAA 1799
 1.5 CITCLIGRAGITTIALGCTTAACSJIJRCARCGTGAGTGAGTTGRATITTATTGTGTTTC 164
 261 AGC: MAGIGCIACAIAAGAIGCIIGIGCIICAIAA 316
 OST WOLLDOOLING SUB-1981
 1c5 AGICCGIAGAGIATIAGCIAACAGAAGCIITUCATIGCCATACIGAGAAGIAGIGGCAGCA 224
 TYPE: nucleic acid
siranuspness: double
 ES TORROGRAMACIOTISMATORARRAMINITERIORIZATOCONTRIBORAÇÃ CARRATATOC 145
 26 CITGCASTGCCTCTGGGTGGAATG SGAGAAATGGAGTGGGTCCACTTCTGTTGTGTTTC 85
 MEDIUM INFE:
 LENGTH:
 MPUTER: IBM PC CUmpatible
 GGCA SEGIGCUIACA 239
 2119 base pairs
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 Conservative
 linear
 Floppy disk
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 MSF Molecuies
 7 48;
 7.6%: Size 29.4; DB 2; Length 2119; 51.1%; Fred. No. 7.9;
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 PCI/US99/08847
 Score 28.8; DE
Pred. No. 12;
U: Mismatches
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 Mismatches
 DB 4; Length 2174;
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RESULT 13 US-09-141-000-2/c Scauence 2, Application US/09141060

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: LENGIH: 500
: TYPE: PRT
: ORGANISM: Human
US-09-141-000-2
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 US-08-ye7-101-36
 CURRENT APPLICATION NUMBER: US/09/141,000 CURRENT FILING DATE: 1938-08-26 NUMBER OF SEQ ID NOS: 30 SUFIWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LEWGIH: 500
 Query Match 7.3%;
Best Local Similarity 9.8%;
Matches 26; Conservative 7
 GENERAL INFORMATION:
 Patent No. 6054295
 Sequence 56, Application US/08967101 Patent No. 5840540
 APPLICANT: Chen, Fang
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
TITLE OF INVENTION: RECEPTOR PROTEINS
 FILE REFERENCE: 19999Y
 GENERAL INFORMATION:
 APPLICANT: ST. GEORGE-HYSLOP, PEIER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
 APPLICATION NUMBER: 08/592,541 FILING DATE: ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 435
 499 IY.MCTY...B..DRCT.TACBWIBS.....A..DBD.YMATYD..S.B....YW... 440
 143 CAGTIGAATTTATTGTGTTICAGTCCGTAGAGTATTAGCTAACAGAAACCITITCLATTS
 259 MTWC..BB..YHT.HG.AA.IM.HC 235
 263 ATCTTCTTGAGGGAAAGAAGCTGAAGTGCTACATAAGATGCTTGTGCTTCATAACTCTCA 322
 STREET:
CITY: E
STATE:
 323 GAAGCIGCAGATTCIGTATAAATCC 347
 83 TITAATCTACAGGAACCCATAACTTCCTGAAGCTITAFGCTTAACAGTGACAACGTGAGT 142
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICATION NUMBER: US/08/967,101 FILING DATE: 10-NOV-1997
 ADDRESSEE:
 COUNTRY:
 SHTYIWINT..K....MDK.BMC..MBSK.D.BTNTTA.Y...A...MCAYW...cv.S '
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 ..RH..T.D..H..M.BT..H..RKSHSNT.T.TM.AB...M.BM.NMRYYG....TYR. G..
 ...CI.YSD..HK.RH.TRB.MHHR..SYRB.C....KWTS...SK.HC.S.SS.C..D
 02110
 Boston
Pitcher, Edmund R
 Massachusetts
 E: TESTA, HURWITZ & THIBEAULT High Street
 183
 77; Mismatches 162;
 Score 28.2;
Pred. No. 10;
 DB 3;
 Length 500;
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; Sequent V 36: %;
; Patent VJ, 590
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 . A de Tobb MYPE: DNA (genomic)
US-us-532-541-38
 RESULT .
 50.00
 TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
TELEPAX: (617) 246-7100
THE PMALION FOR SEQ ID TO 36:
SEQ LANGE CHARACTERISTICS:
TELETATION FOR SEQUENCE ACTOR
STRAIDEL MESS: Single
 Best I hal s
 GENERAL INFORM
 Matches
 TELET MMONIVALI N. CA RMATT N. TELET NATE: (17) 445-700 C. CATALLER NATE: (81) 447-71 N. CATALLER NATE: (81) 451-71 N. CATALLER NATE: (81) 451-451 N. CATAL
 best L. al Similarity 55.8%;
Matches 43; Conservative
 C Mr (15K FEADABLE FORM)

RELIGH LYPE: Floppy di
C Mr (15K FEADABLE FORM)
 # 101-36
477-101-36
 APPLICANT: ROWNENS F-HARMA M
APPLICANT: FRASER, FAUL E
THEL OF INVENTION: GENETIC SEQUENCES AND PROTEINS
THEL OF INVENTION: TO ALZHEINER'S DISEASE
 NAME: Pitcher, Edmand R.
IELLIAMONICATI W INF-RHATI-M:
ILLEPHONE: (617) 246-7000
 S::WARE: PALENTIN Release #1.0, Version #1. CUFFERT APPLICATION DATA:
 NUMBER OF SEQUENCES: 1
CUPPESPONDENCE ADDRESS:
 AIT ShEY/AJENI INFORMATION:
 537 CIGIATAAA DITABA 552
HHH THEFT HE G
 N
1
 ALURESSEE: HI
SIMEEL MAS
ARILICATION NUMBER:
 STREAM PROPERTY STREET
 MELION TYPE: Floppy disk
O'HOTEN: IBM PC COMPATIBLE
HEALTKS SYSTEM: PC-DOS/MS-DOS
 HENSTH: 512 rase pairs
 tal Staild: 15
 ASSIFICATION:
 INFORMATI E:
 4-
31
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 Massar husetts
 Application US/08592511
 High Street lower -
 U.
 Conservative
 ST. GELBIS-HYSL-P, PETER H
ROWNERS F-HARMA M
 bilà (detichila)
 7.2%; Score 28; DB
55.8%; Pred. No. 12;
117e 2: Mismatches
 183
 US/06/594,541
 36.
 2: Mismatches
 Score 28; DB 2;
Pred. No. 12;
 THIBEAULI
125 High Street
 DB 2; Length 512; 12;
 32;
 Length 512
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Search completed: January 2, 2003, 15:06:17 Job time :  $56\ secs$ 

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Result
 Minimum DB
Maximum DB
 scoring table:
 sequence:
 Perfect score:
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 searched:
 Title:
 Database
 Total number
 M nucleic -
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 110554
110554
110554
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result weing printed and is derived by analysis of the total score distribution.
 Score
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37.6
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 35.4
32.8
32.2
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31.8
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Match Length DB
 US-09-762-027-4
388
 113:::
 381593 seqs, 216252194 residues
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 January 2, 2003, 13:45:03
 Published_Applications_NA: *
 GenCore version 5.1.3 Compugen Ltd
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- US-09-833-381-1548
- US-09-925-300-125
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- US-09-960-352-14120
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- US-09-960-352-2495
- US-09-960-352-2495
- US-09-960-352-10521
 US-09-796-692-5227
 ij
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US-09-764-860-966
US-09-764-860-968
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Sequence 134. Apsequence 134. Apsequence 135. Apsequence 5905. Apsequence 6780. Apsequence 6780. Apsequence 6780. Apsequence 6780. Apsequence 1951. Apsequence 5002. Apsequence 5002. Apsequence 209. Apsequence 209. Apsequence 209. Apsequence 507. Apsequence 507. Apsequence 507. Apsequence 507. Apsequence 508. Appsequence 568. Appsequence 568. Appsequence 568. Appsequence 568.
 Description
 Sequence 1550.
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|-----------------------------------------|-------------|-------------------|-------------------|-------------------|---------------------|-------------------|--------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|----------------------|----------------------|-------------------|-------------------|--------------------|---------------------|-------|-------------------|---------|--------------------|
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| to to<br>a a<br>4- 4-                   |             | a)                |                   | •                 | 10 t                | 26                | KV<br>V            | 24.2              | 125.4             |                   | 29.5               |                   | v.                | 4                 | ٥٥                   | J. F.                | ti<br>L           |                   | ر<br>:<br>4ء       |                     | ۵r. a | ;<br>;<br>;       | ÷.      | 0<br>11<br>1       |
| 7                                       | 7           | 7.4               | 7.4               | 7 . :             | 7                   | 7.5               | 7 . =              | 7.5               | 7 . 1             |                   | 7.1                | 7.5               | 7.5               | <br>              | 7.                   | ٠,                   |                   | (1                |                    | n                   |       |                   | (1      |                    |
| un K.                                   | 41.         | 173808            | :157              | 2174              | 000                 | 507               | 577                | :607              | 74565             | 501               | 5215               | $\sim$            | 1 400             |                   | 2000                 | <br>:                | ا<br>             | ال-<br>ديو<br>ديو |                    | ,,                  |       | 1 1<br>10<br>2 1  | :<br>1. | 31.1               |
|                                         |             | i.                | į.                |                   | ٠.                  |                   | Ξ                  |                   |                   | -                 | . <u></u>          | Ξ                 | ų.                |                   | ú                    |                      |                   |                   |                    |                     |       | ٠.                |         | •                  |
| US-U9-761-887-532<br>US-U9-736-457-1361 | 864-761-16  | US-10-003-806+10  | US-10-044-090-765 | US-09-931-087A-4  | US-09-938-842A-4642 | US-09-764-869-535 | US-U9-864-761-8997 | ٠.                | ปร-บ๖-7ช1-558-3   | US-09-963-919-18  | US-05-880-107-1765 | US-09-070-927A-43 | US-10-098-841-103 | 115-vy-773-926-8  | ilS-uy-938-842A-5259 | ils-ilj-y54-456-2086 | 45-09-910-943-513 | 35-09-910-943-218 | 35-19-070-927A-180 | US-19-938-842A-3064 |       | 42h-2             | 10      | 68-19-764-877-2308 |
| Sequence 532, App<br>Sequence 1361, Ap  |             | Sequence 10, Appl | Sequence 765, App | Sequence 4, Appli |                     | Sequence 535, App | Sequence 8597, Ap  | Sequence 551, App | Sequence 3, Appli | Sequence 18, Appl | Sequence 1769, Ap  | Sequence 43, Appl | Sequence 103, App | Sequence 8, Appli | Sequence 5259, Ap    | Sequence 2086, Ap    | Sequence 513, App | Sequence 218, App | Sequence lau, App  | Sequence soca, Ap   | , a   | Sequence 2222, Ap |         | e 230              |

## ALIGNMENIS

US-09-833-381-1950

RESULT 1

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KAME/KEY: misc feature: LOCALION: (1)...(195)
CIHER INFORMALL N: m
US+09+633-381-195:
 : Sequence 1950, Application 05/09853381
: Patent No. 0820020132090A1
 US-09-867-550-929
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 55
 KESULI 2
 ; GENERAL INFORMATION:
 PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-01-19
NUMBER OF SEQ 1D N.S: 205
SOFTWARE: FASUSED for Windows Version 3.0
SEQ 1D NO 1950
LENGTH: 495
Sequence 929, Appli stion Patent No. US200200 92206A) SENERAL INFORMATION:
 Best Local Stailarthy 91/5:
Matches (6: Constructive
 APPLICANT: Robison, Keit, E. 1111E OF INVENTION: No. 052: 20132050Alel Nucleic Acid and Protein Homologs FILE REFERENCE: 5500-115 CURRENT APPLICATION NUMBER: 35/05/633,381 CURRENT FILING DATE: 200:-01:11
 TYPE: DNA
 FEATURE:
 ORGANISM: Homo sapietes
 250 GAAACITCAGAI 261
 THITTITLE T
78 GAAACITCAGGI 89
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 Scare 52: DB 10:
Pred: No. 1.2e-06;
pr Mismatches 5:
 Length 495;
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RESULT 4
US-09-925-300-125
: Sequence 125, A
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 Ę.,
 : FEATURE:

NAME/KEY: misc_reature

LOCATION: (1)...(963)

OTHER INFORMATION: n = A, F, C or
US-09-833-381-1948
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 K
 TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-550-929
 APPLICANI: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homolous
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/05/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 05/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SUFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1548
 • PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID MOS: 2125
SOFTWARE: FASCSEQ for Windows Version 4.0
SEQ ID NO 929
LENGTH: 735
 Sequence 1948, Application US/09833381
Patent No. US20020132090A1
GENERAL INFORMATION:
 Matches
 Query Match
Best Local :
 Matches
 Query Match
 APPLICANT: Topper, James
IITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogener
IITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
 APPLICANT:
APPLICANT:
APPLICANT:
 -05-833-381-1948
 APPLICANT: Leach, Martin D
APPLICANT: Mehraban, Fuad
 ORGANISM: Homo sapiens
 LENGTH: 963
TYPE: DNA
 343 AATCCTTAGAAAAGAGCATCCCCTGAATCCATAAANGTATAINGC 507
 397 AAFCCITGGCCAGGAGCAT+CCCTGAGTCCCTGAAGGIGFAIGGC
 Local Similarity hes 72; Conserv
 Y Match 11.1%; Score 43; DB 10; Lenath 7:
Local Similarity 68.6%; Pred. No. 0.60092;
hes 72; Conservative 0; Mismatches 32; Indeas
 95 CTGAAGCATCCCACAGAATGATCCTACTGAAIAACICCCATAAGCTGUIGGCCCIAIAAA 151
 125, Application US/09925300
 Mehraban, Fuad,
Conley, Pamela
Law, Debbie
 Conservative
 11.1%; Score 43; DB 10; Length v6; 68.6%; Pred. No. 0.001;
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 15-69-925-560-125
 APPLICAMI: Matchalagan, hangtan

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IIILE A INVENTION: MOSTL, AND FAI DEPOSITION

FILE REPRENCE: 17-511, Jul, 17-21 (10/200)C

CUNREN, APPLICATION NUMBER: 08/09/960, 352

CURRENT FILING DATE: 200, 9-24

NUMBER of SEQ ID N St 151, J

SEQ ID NO 8906

LENGTH: 195
 GENERAL HERMANION:
APPLICANI BATTOL MOSTO,
APPLICANI BYATT JOHN C
APPLICANI MATCHELICANI
 Hatches 72: Chiservall
 East Local Similarity
Matches 55; Consert
 Separate 5005, App. Serior Parent No. USzór 20137135A1
 LOCALION: (1041)
COTHER INFORMATION: U.S.
NAME/KEY: m) S. restate
 L CATION: (111)
THER INFORMATION:
OTHER INFORMATION:
 NAME/KEY: un plue
 FEATURE:
 INFE: DNA
 FEATURE:
 RGANISH: Bus Fruit
 MAME/KELL BLEST DESCRIE
 CRGANISM: H....
 LENGIH: 1169
 283 (IIGAAGISCIA DATAAGA, ENLIGIGOTICATAACTOTOAGAAGOTIGDAGATICTGTATA 342 (HILL) | HILL Conservative
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 in the Source 43: DB log Length Flag:
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| - (1)
 1 1
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 Arids, Pluteins
 13/114/125,300
 Score 37.6; DB 10;
Pred. No. 0.023;
 25-11634-068-01-£1-G1
 o: Hismatches
 TID AND WIHER MOLECULES ASS CLAIED WITH LACIATION AND
 Mismatches
 and Antibodies
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Indels

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 US-09-960-352-7792
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 ; TYPE: DNA
; GRGANISM: Bos caurus
; OTHER INFORMATION: Clone ID: 60-L1B34-027-01-E1-G8
US-09-960-352-14120
 RESULT 7
US-09-960-352-14120
 C
 US-09-960-352-7792
 ; Sequence 14120, Applicatio
; Pacent No. US20020137139A1
0
 APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCCLIC ACID AND OTHER MOLECULES ASSACIATED WITH LAGIATION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 14120
LENGTH: 303
TYPER: NAN
 GENERAL INFORMATION:
 GENERAL INFORMATION:
 Sequence 7792, Application US/09960352 Patent No. US20020137139A1
 NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 7752
 APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LANTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21 (10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2011-09-24
 Matches
 Best Local Similarity
 Query Match
 Matches
 APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing
 APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing
 TYPE: DNA
OKGANISM: bos taurus
OTHER INFORMATION: Clone ID: 33-LIB34-076-01-E1-A2
 LENGIH: 313
 156 AGAAATCCTTGAGGAAGAGCCTTCC 182
 340
 280 AAGCTGAAGTGCTACATAAGATGCTTGTGCTTCATAACTCTCAGAAGCTGCAGAITCTGT 359
 280 AAGCIGAAGTGCTACATAAGATGCTTGTGCTTCAIAACTCTCAGAAAOJIGOAGAIICIGI 33×
 Local Similarity
les 55; Conserv
 ATAAATCCTTAGAAAAGAGCATCCC 364
 AGGCTIACGTGTCNTGCATGATGTTCCTGCTGCAAGGTGCCCAGAIGCTGCAGAIGCIGG 157
 AAGGTGAAGTGCTACATAAGATGCTTGTGCTTCAIAACTGTCAGAAGGIGGAGAII:IG:
 ATAAATCCTTAGAAAAGAGCATCCC 364
 AUGCTTACGTGTCTTGCATGTTCCTGCTGCAGGTGCCCAGGTGCTGCAGATGTTGC 211
 Conservative
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 Application US/09960352
 9.5%;
64.7%;
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64.7%;
 Score 37; DB 10; Length 31s; Pred. No. 0.044;
 Score 37; DB 10; Length 353; Pred. No. 0.048;
 Mismatches
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| GRGANISH: POS tâcrus
| OTHER | EC | AMAIICA: Clone | h : 29-11634-011-01-E1-61
| US-09-960-01_ | TBO
 APPLICANI: Mathialagan, Nayappan
ITILE OF INJERTIOR: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION ITILE OF INJERTIOR: MUSCLE AND FAI DEPOSITION
FILE REFERENCE 16511,006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/05/960,352
CURRENT FILENG DATE: 2001-09-24
RUMBER OF SAJ ID NUS: 15112
SEQ ID NU 67-5
LENGTH: 47-5
 Sequence 67 , Articles
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 : GENERAL ILL : MAII W.
 GENERAL INC. MALION:
 Sequence ("s , Apprication US/09960352 Patent No. | S20020137139A1
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 RUMBER OF SELVID KUS: 15112
SEQ ID WC (T)
LENGTH: YOU
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Best Local Similarity 64.7
Matches 57 Conservative
 APPLICAN: byatt. John G.

ARPHICAN: Mathialayan, Nadayyan
IIILE OF INCENTION: NUCLEIC ACID AND GIBER NOLECULES ASSOCIATED WITH LACTATION
IIILE OF INCENTION: MUSCLE AND FAI DEPOSITION
FILE RELEVANCE: 16511.006/37-21(10298)C
CURRENT ASSICIATION NUMBER: US/05/960,352
CURRENT FILENS DATE: 2001-09-24
 APPLICANT: ...rren, Wesley C. APPLICANT: ido, Hengbing APPLICANT: byatt John C.
 LCCALICA:
STHER IA:
STHER IA:
 ORGANISM: 7.5 tadrus
 NAME/KEL.
 FEATURE:
 IMPE: DAM
 183 AGUT. FACGIGITEGCATGATEGTECCIGCIGCAAGGTGCCCAGATGCTGCAGATGCTGC 242
 340 ALABETOCT FAJAAAAGAG 'ATOCC
 280 AAB . JAAGTUDIACAIAAJAIGCIIGIGCIICATAACICTCAGAAGCIGCAGAIICIGI 339
 243 A LABORCOTTGAGGAAGAGCOTTGC 267
 340 ATABATCCTTAJAAAAGAGCATCCC 364
 Similarity 64.7s;
 : (357)
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 . Application Us/09960352
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 9.54;
64.74;
 Score 37; DB 10; Length 379, Pred. No. 0.049;
0; Mismatches 30; Indels
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29-1.1834-001-01-E1-B1
 Score 37;
Pred. No.
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 DB 10;
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 Length 392;
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AA: : GAAGIGCIACATAAGAIGCIIGIGGIIGAIAACTCTCAGAAAGCIGCAGAIICTGI 339

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 ; ORGANISM: BOS TAUTUS
; OTHER INFORMATION: Clone ID: 45-L1634-025-q1-E1-62
US-03-y50-352-10551
 US-09-560-352-10551
 Š
5
 US-09-960-352-2495
 5
 APPLICANT: Warren, Wesley C.
APPLICANT: Hao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC AND FAI DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10551
LENGTH: 399
 Sequence 10551, Application US/09960352
Patent No. US20020137139Al
 Query Match
Best Local Similarity
Matches 55; Conserv
 GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2495
LENGTH: 413
 GENERAL INFORMATION:
 sequence 2495, Application US/09960352
Patent No. US20020137139A1
 Best Local Similarity
Matches 55; Conserv
 Query Match
 APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Machialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER WHENULES ASSEMBLED WITH TAILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511,006/37-21(10268)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
 OTHER INFORMATION: Clone ID: 11-L1834-026-cl-E1-Cl1
 TYPE: DNA
ORGANISM: Bos taurus
 540
 195 AGAAATCCTTGAGGAAGAGCCIICC 219
 340 ATAMATCCTTAGAAAAGAGCATCCC 364
 135 AGGCTTACGTGCATGATGTTCCTGCAGGTGCCCAGATGCTGCAGATGTTGGTGG
 280 AAGCTGAAGTGCTACATAAGATGCTTGTGCTTCATAACTCTCAGAAGCTGCAGATTCTGT 339
 280 AAGCTGAAGTGCTACATAAGATGCTTGTGCTTCAIAACTCTCAJAAGGTGGAGAITCIGI 33×
 ATAAATCCTTAGAAAAGAGCATCCC 364
 AUGCTTACGTGTTGCATGATGTTCCTGCTGCAGGJJGCCCAUAIGCJGCAGAJJCTGG 21
 AUSCITACGTGTCTTGCAFGAIGFTCCTGCTGCAAGGTGCTTAGAFGTICTAJAFGTTTT
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 9.5%;
64.7%;
 9.5%; Score 37; 1:5 10; Length 413; 64.7%; Pred. No. 0.051; ative 0; Mismatches 30; Indels
 0; Mismatches
 Score 37; DB 10
Pred. No. 0.05;
 DB lo: Length 39%;
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APPLICANT MATTERIALS, RESPECT

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FILE METERIAGE 1651.006/37-21(10398)C

CORRECT APPLICATION NUMBER: 08/09/900-352

CORRECT FILES. AND SEE 2001-09-24

RUMBER OF SEC. D. R. S. 15112

SEO ID N. 1202.
 RAME/KEY: unsure
LUCATION: (374)
UNHER INFORMATION:
OTHER INFORMATION:
US-09-9co-352-5co-
 : Sequence 5502, Application
: Putent No. US20-20137139A1
: GENERAL INFORMATION:
 CTHER INFORMATION: Clone ID: US-09-960-352-12-11
 JS-J9-97J-552-1_ _:
: Sequence 12c2i Applitation US/0997∪352
: Putent No. US2 = 2013-139A1
 15 - 19 - 9 10 - 352 - 500
 APPLICANT: Warran, wasley C.
APPLICANT: 180, Nedgbing
APPLICANT: 180, Nedgbing
APPLICANT: Byart, John C.
APPLICANT: Mattisiagan, Hagarpan
HILLE OF INVENTION: NOCLEE CACID AND OTHER MOLECULES ASSOCIATED WITH LACIATION ITHE ST INVENTION: MOSCLE AND FAI DEPOSITION
FILE REFERENCE: 16511.005/37-21(1)258)C
CORRENT FILING AND MOMBER: 05/09/960,352
CORRENT FILING AATIC: 2001-05-21
TUMBER FILING AATIC: 2001-05-21
 GENERAL MECREAL
 best Local :
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Matches 54; Sheet
 Matches
 FEATURE:
 ORGANISM: BOS taut
 340
 159 AGOCTTA NELL FELLEN 180 AAGCIGAAGTGUTACATAAGATGCIIGTGCIICATAACTCTCAGAAGCIGCAGATTCTGI 339
 200 AAGCIGAA MAGCIA TAHAGANGGUIGTGCHCATAACTCTCAGAAGCIGCAGANICIGT 339
163 AGGCTTA GITTGCATGATGTTCCTGCTGCAACGTGCCCAGATGCTGCAGATGCAGG 222
 Local Similarity 64.7
.es 55: Niser/ative
 ATAMATO DITAGAMANGAGCATORC 364
 Application
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hade ID: 24-1.IB34-001-Q1-E1-E7
 54.78;
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3. C. ...
6. C. ...
 51-Lib34-048-01-E1-E4
 Score 37; DB 10; Length 425
Pred. No. 0.051;
u; Mismatches 30; Indels
 Length 374;
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770.445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178.472
PRIOR APPLICATION NUMBER: US 60/178.472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEG ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEG ID NO 209
 Dþ
 US-09-770-445-209
 RESULT 15
US-09-796-692-5227/c
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 20
 : NAME/KEY: misc_feature
LOCATION: (1)...(1022)
: OTHER INFORMATION: n = A.T.C or
US-09-770-445-209
 d
 Sequence 20
Patent No.
 wuery match 8.5%; Best Local Similarity 51.4%; Matches 76; Conservative
 GENERAL INFORMATION:
 Sequence 5227, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:
 APPLICANT:
 APPLICANT:
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APPLICANT:
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APPLICANT:
 APPLICANT:
APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane
 APPLICANT:
 APPLICANT:
 APPLICANT:
 TYPE: DNA ORGANISM: Arabidopsis thaliana
 FEATURE:
 LENGTH: 1022
 333 ATTCTGTATAAATCCTTAGAAAAGAGCA 360
 273 GGGAAAGAAGCTGAAGTGCTACATAAGATGCTTGTGCTTCATAACTCTCAGAAGCTGCAG 333
 213 AAACTGGCAGCAGGCAGTGTGCCTACAGGTCTACAAAGAAACTTCAGAICATCTTCITGA 272
 132 TIATTATACAAATGGAAAAACAAAAGAA 159
 72 AAGACAGGAGCTGAAGTGGTTTATAAATAGATTTTGTACGAAGTTICICIACACAAACCT 131
 12 AAAGTGTTGGAAGAGATTATTATTACACCACAACAAAAAAGACATGATTCACAGTTTGG 71
 209, Application US/09770445
b. US20020023281A1
 Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
Kricker, Maja
Slader, Ted
 An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
 Davis, Keith R.
Allen, Keith
 Yu, Yang
Rameaka, Joshua G.
 Gorlach,
 Matthew, Abraham V.
 Page, Amy
 Jorn
 Score 32.8; DB Pred. No. 1.6; 0; Mismatches
 C
 DB 10; Length 1022;
 72;
 Indels
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FILE REFERENCE AND ANDRESS OF THE REFERENCE APPLICATION NUMBER 50/105/126

PRICE APPLICATION NUMBER 50/105/126

PRICE APPLICATION NUMBER 50/105/126

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## alignments

RiBeck, A.; Reinhardt, K.; Lyne, M.; Rajandreem, M.A.; Barrell, B.; Submitted to the EMB( Nata Librar), october 1998

Araccession: [40eoc A) Reference Lamber: 221949 C:Aucession:

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RESULT 1

hypothetical protein SPBPBB7.12c - fission yeast (Schizosaccharomyces pombe C:Species: Schizosaccharomyces pombe C:Date: 03-DeC-1999 \*Sequence\_recision 03-Dec-1999 \*text\_change 03-Dec-1999

fission yeast (Schizosaccharomyces pombe)

ArStatus: prefiminary: translated from Gb/EMBE/DDBJ ArMolecule type: DMA Arkesidues: 1-220 'BE'  $\mathcal{L}_{i}$ -1 *i*, Percent Similarity: Best Local Similarity: ArCluss-reterences: FM5h:ALouzed): PIMH:(AA21797.1): GSPD5:(H)Jou67: SPD5:SPBP8B7.12c A:Experimental source: Strain 97th-: clone pl p6B7 <u>.</u>;. graety Match: S001 G: Alignment Scores: hidenetics: SS-v9-762-02 -4 (l-see) x ∏4veve (l-22d) Pred. č. ... 151 155 136 (Groad Caste Jaal III al II belli i ragioughagaatatiaghtaacagaaseeti). 195 76 č Srie:Sibras .... CGICTOGTTTA-CCTACAGGAS CCATAACTTCCTGAAGCTTTATGCTTAACAGTGACAA 135 Astribety/searValLeuteutroSerValGinserTieSerSerSer-ASUMIATION OF CONCIONATION AND ASSOCIATION OF CONTROL O 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 10.00 Letigth:
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A; Title: Sequence and analysis of chromosome 2 of the plant A:abidopsis thaliana. A:Reference number: A84420; MUID:20083487; PMID:10517197
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C:Accession: A44890
R:Tawheed, A.R.: Beaudenon, S.: Favre, M.: Orth, G.
J. Clin. Microbiol. 29, 2656-2660, 1991
A:Title: Characterization of human papillomavirus type 66 II.an A.Reference number: A44890; MUID:92129556; PMID:1663315
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A:Experimental source: cultivar Columbia; BAC clone I25K17
C:Genetics:
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Fig. 3455: $27032: $2008: $26756; $26637; $577e3; $64544; $63099
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 r.S.; James, M.G.; Myers,
 31nValProGlyHisCysCysThrAlaSerLeaSerLea
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A;Genome: nuclear (2) A;Genome: nuclear (2) Superfamily: Escherichia coli ribosomal protein L3 (2) Superfamily: Escherichia coli ribosomal protein L3 (2) C;Keywords: mitochondrion; protein biosynthesis; ribosome F;1-19/Domain: transit peptide (mitochondrion) *status experimental *:NF/F;20-269/Product: ribosomal protein L3, mitochondrial *status experimenta
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A.Residues: EMBL:Z73004: NID:gl323394; PIDN:CAAy7248.1: PIT:g
A.Experimental source: strain S288C
R:van der Aart, Q.J.M.; Kleine, K.; Steensma, H.Y.
Yeast 12, 383-390, 1996
A.Fitle: Sequence analysis of the 43 kb CRM1-YLM9-PEI54-DIE2-SMI1-FH
A.Reference number: S63896; MUID:$6267763; PMID:8701610
A.Recession: S63896
 A:Molecule type: protein
A:Residues: 176, TF, 179-182;257-261 <GRO>
R:Van der Aart, O.J.M.; Kleine, K.; Steensma, H.Y.
Submitted to the EMBL Data Library, June 1995
S.Description: Sequence analysis of the 43 KB CKMI
A:Reference number: $57680
A:Accession: $57683
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 A:Gene: SGD:MRPL9; YML9; MIPS:YGR220c
A:Cross-references: SGD:S0003452; MIPS:YGR220c
A:Map position: 7R
 A:Title: Extended N-terminal sequencing of A:Reference number: S17255; MUID:$1285106; A:Accession: S26637
 A:Experimental source: strain 07173
A:Note: this sequence has been revised in reference
R:Grodimann, L.; Graack, H.R.; Kruft, V.; Choli, T.;
FEBS Lett. 284, 51-56, 1991
 A:Title: Mitochondrial ribosomes of yeast: A:Reference number: $26754; MUID:89078618; A:Accession: $26756
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 A; Note: the nucleotide C; Genetics:
 A;Cross-references: EMBL:x87941; NID:g886508; PIDN:CAA611>d.1; A;Note: the nucleotide sequence was submitted to the EMBL fata
 A; Molecule type: DNA
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A;Accession: S64544
 A;Cross-references: EMBL:X87941; NID:g88650b; PfDN:CAA611'd.1; A;Experimental source: strain S288C R;van der Aart, Q.J.M.; Steensma, H.Y.
 A; Molecule type: DNA
A; Residues: 1-269 < VAN>
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 le: Characterization of the Cephalosportum acromonium (chab deby stillis) i aquas so of early cephalosporin biosynthetic genes and evidence of multiple for Nicola doma serence number: A38531; MOID:91177827; PMID:1706706
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A; Accession: A10336
A; Status: preliminary
A; Molecule type: DNA
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A:Authors: Mueller-Auer, S.; Silvey, M.; James, K.; Montfort, A.; Poils A.; Ligding erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Bengs, V.; Periman, S.;
C:Chalkatis, N.
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C.Date: 21-Dec-1996 *sequence_revision 06-Jun-1997 *Lext_change 20-Jun-2200
C.Accession: G01646
R.Bowdish, K.S.
 submitted to the EMBL Data Library, January 1995
A; Reference number: G08025
A; Accession: G01646
A; Status: preliminary; translated from GB/EMBL/DDBJ
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 Alignment Scores: Pred. No.:
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Search completed: January
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 A;Cross-references: EMBL:U20285; NID:g644878; PIDN:AAC50906.1; PID:y644a79
 236 LeuGlyValLysSerCysIle 242
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 298 ValAlaIleTyr 301
 282 AlaSerPheAspHisCysAspPhe------Pro---GluLeuLeuSerProserAst 257
 262 AlaGlyLeuAlaGluLeuAlaAlaArgLysTyrLysGlnAlaAlaLysCysLeuLeuLeu
 271 GAGGGAAAG-----
 222 GlnAsnTrpSerHisValLeuSerTyrValSerLysAlaGluSerThrProGluIleAls 24i
 211 AGAAACTGGCAGCAGGCAGTGTGCCTACAGGTCTACAAAGAAACTTCAGATCATCTTCTT 270
 103 AACTTCCTGAAGCTTTATGCTTAACAGTGACAACGTGAGTCAGTTGAATTITATTGIGIT 182
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 112892 seqs, 41476328 residues
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| EMBL: X02819: "AA26587:1: ".<br>EMBL: X54421: "AA36288:1: ". | This SWISS-PF centry is copyright. It is produced through a collaboration between the Siss Institute of Bioinformatics and the Eval outstation the European B. Hardrautics Institute. There are no restrictions on its use by non-point institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a linease agreement (See http://www.isb-sib.cm/announce/or send an education of linease agreement (See http://www.isb-sib.cm/announce/or send agreement (See http://www.isb-sib.cm/announce/or se | Lang b.F.;<br>S.LBAITEEU (AUI 1970) to the EMBL/Jenbank/DDBJ databases,<br>11- MISCELLAME 75: THE EXCIPIN IS CODED IN THE GROUP-II THIKON OF<br>Cos.<br>11- SEMILARED - 10 GROUP II THIKON MATURASES. | Tirst two list is in the savelatomyles deferishes coal general Mot. Bio. 194:359-77 (1985).  [2] SEQUENCE E. M. N.A. SIRAIN AD7-5.1                                                                                                 | SEQUENCE FROM N.A.  SERAIN-AD7-50: S | Schizosaccharoly es poure (fission )ease/. Mitochondrio. Eukarylla, Eurli Asconyola: Schizosaccharomycetes: Schizos.Locharolycetales: Schizosaccharomycetaceae: Schizosaccharolyces. Kibl_FisiD=469: | RESULT i  VM31_SCHPC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

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 riam: P:00518; E6: 1.
Early protein; DNA-binding; Na ZH FING 33 69
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 This SWISS-PROT entry is copyright. It is produced thrown a Collaboration between the Swiss Institute of Bioinformatics and the EMBL Swistlet. It the European Bioinformatics Institute. There are no restrictions of the by non-profit institutions as in the are not institutions as its voltant is in the modified and this statement is not removed. Usage by and for collaboration entities requires a license agreement (See http://www.isb-glo.ch/sch.n.w/or send an email to licensedsb-sib.ch).
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Pfam; PF01348; Intron_maturas2;
SMARI; SM05507; HNHC; 1.
 InterPro:
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 Submitted (OCT-1995) to the -i- FUNCTION: EXHIBIT A STRO SIRANDED DNA (IN VITRO).
 Viruses: dsDNA viruses, Fapill.mavirus.
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 Human pupillomavirus type
 Hypothetical protein; Mitochondrion SEQUENCE 807 AA; 91637 MW; AFD7
 EMBL; U31794; AAA79499.1;
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 NUBI_FaxID-37119;
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 SUBCELLULAR LOCATION: Nuclear matrix-associated
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 CysClnSerThrTyrLysValGluMetHisHisValArgGluMetLysAsaLeuLysFro
 TGCCTACAGGTCTACAAAGAAACTTCAGATCATCTTCTTGAGGGAAAGAAGGTGAAGTGC
 AGAGTATTAGCTAACAGAAACCTTTCCATLGCCATACTGAGAAAG1650CAGGCAGGCAGTG
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 TACATAAGATGCTTGTGCTTCATAACTCTCAGAAGC----
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15-JUL-1959 (Rel. 38, Last annotation update)
60S ribosomal protein L9, mitochondrial precursor (Ymis).
MRPL5 OR YGR220C OR G8520.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina: Saccharomycetes:
Saccharomycetales; Saccharomycetaceae: Saccharomyces.
 TIGREAMS; TIGR01305; GMP_reduct_1; 1.

PROSITE: P$00487; IMP_DH_GMP_RED; 1.

OXIGOTEGUCTASE; NADP; Complete proteome.

BINDING 186 186 1MP (POTEMPIAL).

NP_BIND 216 239 NADP (POTEMPIAL).

SEQUENCE 349 AA; 38319 MM; D4D109E05B493072
 "YmL5, a nucleus-encoded mitochondrial ribosomal protein of yeast, homologous to L3 ribosomal proteins from all natural kingdoms and photosynthetic organelles.";
Eur. J. Biochem. 206:373-380(1992).
 STRAIN-S288c;
MEDLINE-96267763; PubMed-8701610;
 SEQUENCE FROM N.A
 MEDLINE=92283262; PubMed=1597181;
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01-OCT-1996 (Rel. 34,
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 InterPro; IPR001093; IMP
Pram; PF00478; IMPDH_C;
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 STRAIN-07173
 NCBI_TaxID=4932;
 KM09_YEAST
 InterPro; IPR003009; FMN_enzyme.
 178
 i36 GluHisIleValSerPheLeuLysLeu 144
 116 IlePheLeuLeuSerSerGluLeuLysTyrIleCysIleAspValAlaAsnGlyTyrSer
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 22 ITCTCAGTCCTCCTGGTCTACAAAGCCTGTGA1TICITGT-----CIAIGG
 GATCATCTTCTTGAGGGAAAGAAGCTG
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 ACAGAACGTCTGGTTTAATCTACAGGAACCCCATAACTICCJG------AAGCTI 117
 TyrSerAlaSerIleTrpSerGlyIleProIleIleAlaAlaAsnMetAspIhrIleGl;
 LeuAsnHisValIleValSerIleGlyThrSerAsnIleAspPheLeuLysIleLysLys
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Pfam; PF00270; DEAD; 2.
Pfam; PF00289; Sec63; 2.
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SMARI; SMU0487; HELICC; 1.
 Hypochetical protein; Helicase; m spliceosome; Nuclear protein; AIF 20MAIN 457 897 1. LOWAIN 1344 1738 11. LOWAIN 457 504 ATP SITE 609 612 DEIH SITE 609 612 DEIH SITE 1448 1451 DDLH ELAMAIN 221 228 POLY
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Y46G5A.4.
 ;-762-027-4 (1-388) x U520_CAEEL (1-2145)
 SEQUENCE
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 Submitted (JUL-1999) to the EMBL/GenBank/UJBJ databases ::- FUNCTION: PUTATIVE RNA HELICASE INVOLVED IN THE SESPLICING (BY SIMILARITY).
 Eukaryota; Metazoa;
Rhabditidae; Peloder
 Wallis J.M.;
 SIRAIN-Bristol N2;
 SEQUENCE FROM N.A
 Caenorhabuitis elegans
 1123
 EMBL; AL110485; CAB60351.1; -.
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small inducible cytokine Al6 precursor (CCL16) (IL-10-inducible chemokine) (Chemokine LEC) (Liver-expressed chemokine) (Monotactic-1)
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 MEDLINE-98261451; PubMed-9596672; Hedrick J.A., Helms A., Vicari A., Zlotnik "Characterization of a novel CC chemokine, increased by interleukin-10."; Blood 51:4242-4247(1996).
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Yoshite O., Nomiyama H.;
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Biochim. Biophys. Acta 1396:273-277(1994).
 NCB1_TaxID=9606;
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 Warch J., isnikawa F.;
"spRapt and spRint, recruited to telomeres
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Sitson R., Merking D., Mills S.D., Jiang Q., Taylor D.E., Voris
 "Generate sequence comparison of two unrelated isolates of the human gastic pathogen Hellocharter pylori.":
Nature 397:176-e-0(1999).
-i- SIMILARITY: BELONGS TO THE UPPU004 FAMILY.
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 TIGKEAMS: IIGKOLVEST, ÜPFOUUT: 1
PROSTIE: PSU1276; ÜPFOUUT: 1
Hypothetical pritein; Compute profeome.
SEQUEDIE: 437 AA; 49423 MW; 3F14A59AF9FE2B51
 EMBE: AEGO1463; AAGO5046.1; -
 This SWISS-PROJ entry is copyright. It is produced through a collaboration between the Salss Institute of Bioinformatics and the EMBL outstation -
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 NCBI_TaxID-859f ::
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 220 CAGCAGGCAGI IN ECCTACAGGICTACAAAGAAACTICAGAICATCITCIIGAGGGAAAG
 163 10AULUSTA HATTAITAGUTAAGAJAAGCUTTUC---AIIGCGATAGIGAGAAACIGG
 dinLysLysAlainnIleArgSerLeuLeuAsnIleSerIleGlyGysAspLysLysCys
 AGATICISTA: SAAICCITASAAAAGAGCATCCCCTGAATCCATA
 GluLysalaVal HuValAlaIleAspTyrAspGluSerAlaTyrAlaFneGluFneFhe
 betValSerticeValleuGlyAlaArgAshValSerLystleSerGlnValHeHisLys 112
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Fomb J.-F., White O., Kerlavang A.K., Clayton k.A., Sutton d.3., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Fougherty B., Peleson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Cotton M.D., Weldman J.M., Fujii C., Bowman C., Watthey L., Wallin Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Venter J.C.;
 GCH2_HELPJ
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 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for connercial entities requires a license agreement (See http://www.isb-sic.oh/announce/or send an email to licensee/isb-sib.ch)
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HYPOTHECICAL PROTEIN; Complete p
 EMBL: AE000546; AAD07337.1; -.
TIGR: HP0269; -.
Interpro: IPR001861; UPF0004.
Pfam: PF00919; UPF0004; 1
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 SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
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 Hypothetical protein; SEQUENCE 437 AA; 4
 pylori.";
Nature 386:539-547(1997)
 Helicobacter pylori (Campylobacter pylori).
Bacteria: Proteobacteria; epsilon subairision;
 01-NOV-1557
16-OCT-2001
 -!- SIMILARITY: BELONGS TO THE UPF0004 FAMILY
 "The complete genome sequence of the
 Hypothetical
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 153
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 GluLysAlaValGluValAlaIleAspryrAspGluSerAlaTyrAlaFheGluFheFno
 {\tt SerValSerPheValLeuGlyAlaArgAsnValSerLysIleSerGlnValIleHisLys}
 AlaTyrCysIleValProHisThrArgGlyLysGluIleSerIle
 AGATTCTGTATAAATCCTTAGAAAAGAGCATCCCCTGAATCCATA
 GluLysLysAlaGlnIleArgSerLeuLcuAsnlleSerTleolyCysAspLysLysCys
 AAGCTGAAGTGCTACATAAGATGCITGTGCTTCATAACTCTC-----AGAAGGTGG
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 "Genomic Sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";

Nature 397:176-180(1999).
-I- CATAKYTIC ACHIVITY: GIP - 3 H(2)0 - formate + 2,5-diamino-6-hydrox; (4-(5-phosphorito-sylamino)pyrimidine + diphosphate.
-I- PATHWAY: Riboflavin biosynthesis; first step.
-I- SIMILAPITY: BELONIS TO THE GIP CYCLOHYDROLASE II FAMILY.
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"F., idemiology of influenza C vitus in man: multiple evolutionar;
illusayes and low rate of change.";
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N'bi_TaxID=11508;
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...cerpro; IPR005188; Flu_C_NS2.
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EA Eagguley C., Baikey S.E., Bridgeman A.M., Buck D., Burgess J.,
EA Conroy D., Corby N.R., Cobley C.C., Coller R.E., Connor R.,
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EA Hartyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCain O.T.,
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EA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith H.L.,
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EA Hunds K., Kemp G., Chissoe S., Murray J., Miller N., Milley D.,
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EA Enanuel B.S., Shakh T., Kurahashi H., Satta S., Buderr M.,
EA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedta D.,
EA Scroussi E., Fransson I., Tapla I., Bruder C.E., O'Frien K.P.,
EA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedta D.,
EA Script C.E., Gebrus C., Lance L.,
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 HM21_HUMAN STANDARD; PRT; 599 AA.

Q9UGU5; Q9UMT5; Q75673; Q75672;

16-QCT-2001 (Rel. 40, Created)

16-QCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

High-mobility group protein 2-like 1 (HMGBCG protein).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Homo sapiens (Human)
 HMG2L1 OR HMGBCG
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MEDLINE=99263500; PubMed=10329004; Seroussi E., Kedra D., Kost-Alimova M., Sandberg-Nordqvist A. C., Fransson I., Jacobs J.F., Fu Y., Pan H. Q., Roe B.A., Imreh S.,
 Wilkinson P., Bodenteich A., Hartman K., Hu
Tilahun Y., Wright H.;
"The DNA sequence of human chromosome 22.";
Nature 402:489-495(1999).
 Submitted (JUN-1999)
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Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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 JS-Ü9-762-Ü27-4 (1-388) x AAB85771 (1-294)
 11-FEB-2000;
17-FEB-2000;
25-FEB-2000;
03-MAR-2000;
09-MAR-2000;
 (INCY-) INCYTE GENOMICS INC
 08-FEB-2001:
 inflammatory, cell proliferative, developmental, endocrine such as aneurysm, eye, metabolic, and gastrointestinal disorders, including lived disorders and infection. The present sequence represents a human DME.
 The invention provides human drug metabolizing enzymes (DME) and polynoclectides encoding the DMEs. The DME can be expressed by standard recombinant methodology. DMEs and their agonists and antagonists are useful for the diagnosis, treatment, and prevention of autoimmune/
 rsolated polypeptide encoding a drug metabolizing enzyme useful for to diagnosis, treatment, and prevention of autoimmune/inflammatory, cell proliferative, developmental and endocrine disorders.
 Claim
 17-MAR-2000;
 Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; inmunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynascological; antibacterial; gene therapy; neural; immune; reproductive; renal;
 Human prostate cancer antigen protein sequence SEQ ID No: 105
 AAB56487 standard; Protein;
 Match:
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 gastrointestinal;
 13-MAR-2001
 AAB56487
 wound; intectious disease
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DB; AAH76198.
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 Page 130; 150pp; English.
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2000US-0185141.
2000US-0186818.
2000US-0188345.
2000US-0189997.
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 2001WO-US04423
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93.10%
17.81%
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 cardioactive, inm...omodulatory, muscular, vulnerary gastrointestinal, nephrotropic, antinfective, gynaecological and antibacterial activities, and can be used in yene therapy. The prostate cancer antigen polynucleatides may be used for detection of prostate cancer, encomposine identification, as chromosome markers, and for numerous other diagnostic or research, purposes. The prostate cancer antigens may be used in treat disolders such as heriral, innume, muscular, reproductive.
 Prostate rancer arsociated dene sequences, referred to as prostate cancer antiques. Setul for treatment, prevention, and diagnosis of disorders such as prostate vancer \dot{}
 distrointestinal.
distracts, Woulds
 proteins, called prostate cancer antigens, given in AAB56363 to Ad
The prostate cancer antigens can have neuroprotective, cycostatic,
 AAF15566 to AAF16735 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302
 Claim 11; Page 14-c-1489; 2336pp; English
 N PSI h:
 (BUSE/) R.SEN
 (HUMA) HIMAN
 12-MAK-1999;
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 TI-Speciality
 Ckheta-12: hachat poietic: cancer: Chemotherapy; leukachia: pauriasis: tumour; i-cell meriated autolumnum disease; liver cirrhosis: catedarthintis: plmonary fibrosis: schistosomiasis; trichinosis: ascailasis; prostuglandin-independent rever; silicosis; rheumatoid arthriis: hyper-eusinophilic syndrome.
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 78-09-701-027-4 (1-388) x AAW06575 (1-136)
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 Peptide
 (BEMA-) HUMAN GENOME SCI INC. (SMIK) SMITHKLINE BEECHAM CORP.
 υι - JUN-1995;
 Claim 1; Page 43; 55pp; English
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 211 -----AGAAACTGGCAGCAGGCAGTGTGCCTACAGGTCTAC---AAAGAAAGT1 'AGA1 26
 196 TCCATTGCCATACTG-----
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DB; AAT49221.
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 SerLeuLeuValLeuIleLeuIleIleThrSerAlaSerArgSerGlnProL;sVaiPro
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 occurring genomic sequences. HIFS, tragments are useful for screening
 HTFS, or in assays to monitor patients being treated with Hits of agonists, antagonists or inhibitors of HTFS. The present set while
 10-SEP-2001; 2001WO-US26015
 21-MAR-2002
 WO200222660-A2
 expressed sequence
 neuroprotective;
 antiinfertility;
 Novel human
 27-JUN-2002
 ABB97238;
 ABE97238 standard; Protein;
 Sequence
 represents an HTFS
 used
The present invention provides the protein and coding sequences of the novel human proteins. These were isolated from expressed sequences tags (ESIS). They can be used to stimulate cell growth, to regulate the haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth, e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat
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 11-SEP-2000; 2000US-0659671
 An isolated polynucleotide for treating diseases associated encoded polypeptide such as cancer and multiple sclerosis -
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 Example 2;
 (HYSE-) HYSEQ INC
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 rring genomic sequences. HIFS, and its catalytic or has accepted meants are useful for screening libraries of compounds in a carlety as screening techniques. Annibodies which specifically blue air's fail by for the diagnosis of disorders associated with the expression of
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 2002-292408/33.
 antianaemic; vulnerary; antiinflammatory; immunomodulator;
fertility; cerebroprotective; cytostatic; rheumatic; yene therapy;
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Yang Y,
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 US-119-762-027-4 (1-388) x ABB07518 (1-302)
 Percent Similarity:
Best Local Similarity:
 arthritis, atopic dermatitis, glomerulonephritis and initiable bower syndrome, trauma, and bacterial, viral, parasitic, produced, fungal, halminthic infections), cell proliferative (e.g. cancer, atherosciler sistand hepatitis), developmental (e.g. cerebral palsy and cataract), and hepatitis), developmental (e.g. cerebral palsy and cataract), ynecomastia), eye (e.g. iritis and glaucoma, metabolic (e.g. addisc. silsease, diabetes and obesity), and gastrointestinal disorders (e.g. alsease, diabetes, and obesity), and gastrointestinal disorders (e.g. anorexia, nausea, abdominal angina, ulcerative colitis, diarrhoea and constipation). The DME polypeptides are useful in drug screening rechniques, and to analyse the proteome of a tissue or cell type. The fME polynucleotides are useful for creating knock-in humanized animals or model human diseases, and in somatic or germline gene therapy. The present sequence represents a human DME polypetide
 and polynuclectides. DMEs can be expressed by standard recombinant methodology. The DME polypeptides, polynucleotides, mcdulators and antibodies are useful from diagnosing, treating and preventing autoi...../inflammatory (e.g. allergies, anemia, asthma, osceptorosis, theumat...)
 Sequence
 antiarthritic;
 antiarteriosclerotic; vasotropic; immunosuppressive; antirheumatic,
 antiinflammatory;
 OX2R protein; OX2RH1;
 kat OX2R polypeptide
 19-MAR-2001
 AAB48010;
 AAB48010 standard; Protein;
 15-MAY-1999;
03-NOV-1999;
 kattus rattus
 11-MAY-2000; 2000WO-US12998
 WG200070045-A1
 Match:
 (MEDI-) MEDICAL
 Peptide
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 360 ATCCCCTGAATCCATAAANGTATAT
 21
 invention provides human drug metabolizing enzyme (DME) polypeptities
 scores
 Ile-ProGluSerLeuLysValTyr
 302
 (first entry)
 gene therapy; rat.
 AA;
 99GB-0011123
99GB-0025585
 /note= "signal peptide"
25..327
 Location/Qualifiers
 RH1; OX2RH2; OX2RH3; OX2RH4; OX2RH1.2;
cytostatic; neuroprotective; nootropic
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72.00
82.76%
55.17%
10.96%
23
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 Alignment Scores:
Pred. No.:
 US-09-762-027-4 (1-508) x AAB48010 (1-327)
 Query Match:
best Local Similarity:
 Percent Similarity
 The invention calates to rodent or primate OX2k proteins, especially OX2RH1, OX2RH2, OX2RH3, OX2RH1, or OX2RH1.2 proteins. Agonists and antagonists of the OX2kH sequences can be used to modulate physiology or development of a cell, particularly for enhancing mysiolid function or enhancing immunity. The sequences can be used to identify non-OX2 ligands for an OX2k. The polypeptides and polynucleotides can be used to treat inflammatory. Eukoproliterative, neurodegenerative or post-traumatic conditions, in luding atherosclerosis, multiple sclerosis, ischaemia, neurodegeneration, rheumatoid arthritis, and autoimmunity. The present sequence represents the rat OX2k polypeptide.
 Manmalian \cos 2\theta proteins and DHA sequences useful for modulating the physiology and development of a cell -
 Cherwinski n
 Barcla;
 (SCHE) SCHERICA CURP
 Sequence
 Abboso5c standard:
 23-MAR-2001; 2001W0-US09251.
 WJ20v17" v42-Az
 Brusophila
 ABBÓJÓSÓ:
 27 - SEP - 2001
 Drosophila melinogaster
 Prosophila: de elopmental biology; cell signalling; insecticide;
 26 - MAR - 2002
 ري
د د د
 212
 247
 154 TATTGTGT1.CAGTCCGTAGASTATTAGCTAACAGAAACCTTTCCATTGCCATACTGAGA
 207 LysCysLysLeuProLysSerGlyAlaThrProAsp 278
 PhecysValValSerHisLeuThrThrGlyAsnGlnSerLeuSerIleGluLeuGlyArg
 TICTGTATAAATCCTTAGAAAAGAGCATGCCGTGAA 369
 GlyGlyasplinLeuLeuGlySerTyrTle-----
 2001-01-2-1/02
 AACTGGCAG "AGGCAGTGTGCCTACAGGTCTACAAAGAAACTTCAGATCATCTTCTTGAG
 SerTleIleIleLeulleIleIleGiyCysIleCysLeuLeuLysIleSerGlyCysArg
 GGAAAGAAG TIGAAGIGUTACAIAAGA GCIIGIGCTTCATAACICTCAGAAGCIGCAGA
 AAJB41-5,
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Phillips
 (fille peril)
 21-22: 142pp: English.
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 JH. HOEN KM,
 polypeptide SEQ ID NO 17760
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 Gaps:
 Mismatches:
Indels:
 Conservative:
 Lanier LL, Kri
m, Sedgwick JD:
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 Wright GJ;
 -GlniyrIleIlePro
 333
 231
 213
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 273
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RESULI 9
ABB62231
ID ABB6
XX ABB6
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XX ABB6
XX Z6-5
XX Z6-5
XX DFG DFG
 Percent Similarity:
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 US-09-762-027-4 (1-388) x
 Alignment Scores: Pred. No.:
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical usugs. The insection discloses genomic DNA sequences (ABL10176-ABL30511), expressed LNA sequences (ABL01076-ABL30511), expressed LNA sequences (ABL01076) and the encoded proteins
 11-JUL-2000;
 23-MAR-2000;
 (PEKE) PE CORP NY
 Disclosure; SEQ ID NO 17760; 21pp + Sequence Listing; English
 genes from Drosophila
interactions .
 New isolated nucleic acid
genes from Drosophila and
 Drosophila
 Sequence
 at ftp.wipo.int/pub/published_pct_sequences
 specification,
 26-MAR-2002
 ABB62231 standard;
 (ABB57737-ABB72072)
 133
 207
 283
 187
 167
 184
 150
 138
 122
 73
 13 CGGAACATATTCTCAGTCCTCCTCTGGTCTACAAAGCCTGTGAITTCTTGTGTAIGAGA
 sequence data for this patent did not form part of the printer
diffication, but was obtained in electronic format directly from
 2001-656860/75.
 CAACGTGAGTCAGTTGAATTTTATIGIGTTTCAGTCCGTAGAJTATIAGCT---
 ArgAsnIlePhe-----LeuLeuPheAlaLeuProTrplleLeuThrPh.eVai-----
 GluLeuGlnGlyLeuPheTrpHisArgSerThrSerValThrLeuIleProTyrTrpSer
 GAACGTCTGGTTTAATCTACAGGAACCCATAACTTCCTGAAGCTTTATGCTTAACAGTGA
 ValTyrSerAlaValAsnIleIleIleLeuTyrThrMetAry
 CTGAAGTGCTACATAAGATGCTTGTGCTTCATAACTCTCAGA 324
 GlnIleIleGlyGlyGlyValSerLeuGluLysAlaSerHisLeuSerGl; AsnSerArg
 CAGGCAGTGTGCCTACAGGTCTACAAAGAAACTTCAGATCAICIICIIGAGGGAAAGAAG
 -----ValileGinHisPheCysileSerAsnTrpArgAlaileGinLeufyrGly
 1229
 melanogaster polypeptide
 ------AlaSerGlyLeuIleAsnTyrIleAryFheIjrMeL------
 Adams M,
 2000US-191637P
2000US-0614150
 (first entry)
 -----AACAGAAACCTTTCCATTGCCATACTGAGAAACTGGCAG
 AA;
 2.84
68.50
43.86%
19.30%
10.43%
 Protein;
 ABB63656 (1-1229)
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 Length:
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Mismatches:
Indels:
 Gaps:
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phan senti
 capable of detecting to have genes from prosophile. The inventuageful in development is tology and in delidating cell signalling cell-cell interaction. In higher envaryones for the development of insecticides, therapolities and pharmaceutical drugs. The invention discloses generate DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABL30737-ASB*1072).
 Line philip herein
 Abbé4470 stanion
 2240
 The segmence data for this patient did not form specification, but was abrahaed in electronic mat ftp.wipo.int/pub/p.blished_pct_segmences.
 11.6
 Disclosure: Si, h h
 New isolated thereto
genes from Eros politi
 EF ::
 (PEKE) PL .
 23-MAR-2000: Low 08-11-15-11.
11-30E-2000: Low 08-11-14-50.
 27-31.6-2001.
 W0200171042-AL
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 Seyuan, a
 interactions -
 Venter
 23-MAR-2001:
 brosophila; developmentar biology; cell signalling; insecticide;
 Drosophila metaloriastic p Typeptide Sby
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 invention relates t
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Sb: ABL∪6>+1.
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 ...: Jetection reagent for detecting
and for elucidating cell signalling
 .54a5: 21pp - Sequence Listing: English.
 an isomated nucleic acid detection reagent
or more genes from Drosophila. The invent

 reli signalling: insecticide;

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 (1-2441)
 Myers
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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 ID NO 20202
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 The invention
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 Best Local Similarity:
Query Match:
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 US-09-762-027-4 (1-388) x ABB64470 (1-463)
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 Percent Similarity:
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RESULT 11
 useful in developmental biology and in elucidating will simulting cell-cell interactions in higher ewaryones for the development of insecticides, therapeutics and pharmaceutical drugs, the invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABC0721). The sequence (ABL01840-ABL16175) and the encoded proteins
 WO200171042-A2
 Drosophila melanogaster.
 New isolated nucleic acid genes from Drosophila and
 23-MAR-2000;
11-JUL-2000;
 23-MAR-2001; 2001WO-US09231.
 The sequence data for this patent did not form park of the printed specification, but was obtained in electronic format directly from
 Disclosure; SEQ ID NO 20202; 21pp + Sequence Listing: English.
 Venter JC, Adams M,
 at itp.wipo.int/pub/published_pct_sequences
 interactions
 NO . .
 144
 289
 134
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 250
 337
 255
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 7.1
 14 GGAACATATTCTCAGTCCTCCTCTGGTCTACAAAGCCTGTGATTTGTTGTGTATJJACAG
 2001-656860/75
 GATGCTTGTGCTTCATAACTCTCAGAAGCTGCAGATTCTGTATAAA! 345
 AACGTCTGGTTTAATCTACAGGAACCCATAACTTCCTGAAGCTTTATGCTTAA CAGTGAC
 GlyGlnHisAlaProGlyAsnSerGlyLeuLysGlyPhefrpLeuIhrValValGluSer 269
 TTTCCATTGCCATACTGAGAAACTGGCAGCAGCAGTGTGCCTACAGATATAAAAAAA
 AACGTGAGTCAGTTGAATTTTATTGIGTTTCAGTCCGTAGAGIAIIAGCIAACAGAGAACC
 SerValTrpPheGlyPheProIleGluVal-ValProHisserArdIhrAstValAtaVa
 luCysGlnGlnArgTyrLeuLeuArgTyrCysAsnCysThrValAsp
 luSerGluHisPheArgThrLeuGluGlyGlnLysTyrMetLeuGluAsnCysGithAlaG
 CITCAGATCATCIT -----CTTGAGGGAAAGAAGCTG-----AA;IGCIA 'AIAA
 --ThrLeuSerLeuProSerSerTrpArgHis-----CysValMctAsplyrit.GluG
 lThrAlaVal-TyrHisTyrPheAspGluSer-----
 from Drosophila
actions -
) PE
 ABL08573
 CORP NY.
 463 AA;
 2000US-191637P
2000US-0614150
 2.82
67.50
41.88%
23.08%
10.27%
 Ľ.
 PWD,
 detection reagent for detecting for elucidating cell signalling
 Myers
 Matches:
Conservative:
 Indels:
 Mismatches:
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Lery Match:
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 best Local Similarity:
 The invention relates in isolated polynucleotide (1) and polyperation (11) sequences. (1) is useful as hybridisation probes, polyperase mainty feaching (rek) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping and in recombinant production of (II). The continuous control is useful in gene therapy techniques to restore formal activity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore formal activity of (II) or to treat disease states involving (II). (II) is useful in tissue, as molecular weight markers and as a food supplement (I), and its binding partners are useful in medical a food supplement. (I), and its binding partners are useful for treating or quantification of sites capitally (II). (I) and (II) are useful for treating distances involving an irrent protein expression or biological activity. The properties of interpretation of mutations in responsition foresists, when mapping identification of mutations responsition foresists, when mapping identification of mutations responsition of genetic distributions to the primer of the products dependent on DNA and distant still annotion and a classification of the invention.

Note: the sequences, abb00010-ABG30377 represent note branch from WIPO at III, with a find a classification of the printed specification of the prin
 percent Similarity:
 Arrigidant S
 AB 1241.14 Francist 1
 31-MAR-2000 0
23-AU3-2 1 1
 W029-1175047-A2
 food suppressent; medi:
 Rozel haman diada St.
 New isolated political transfer of the section of t
 W-Est n:
 1. T. . .
 Dradau. RI
 30-MAR-2
 11-21-20
 Homo suprema.
 le-Fibers
 Claim 20: SEQ ID No Endes: 103pp: English.
 responsible for accel-
 (HYSE) HYSEV II
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 01-139362/71.
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 2001% 1-11:
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 71
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 The and encoded polypeptides, useful in
tene mapping, identification of mutation
insorders or other traits and to assess

 ...; yene mapping; gene therapy; forensic;
... imaging; diagnostic; genetic disorder.
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 # 24115
 7
 Mismatches:
Indels:
 Length:
Matches:
Conservative:
 Gaps:
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18-09-762-027-4

(1-3dg)

x Andr4124 (1-203)

279 GAAST GAAAGGCTACATAAGAASATSULTGTGGCTGCATAAGCCGCCAGAAGCTGCAGAAGTTCTG

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3
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 RESULT 1.
Percent Similarity:
Best Ibral Similarity:
 Aliquacut Scores:
 purpopose (II) sequences. (I) is useful as hybridisation prices purpopose chain reaction (PCR) primers, obliquates, and for carcastic and gene mapping, and in recombinant production of (II). The relativity of the restore normal activity of (II) or to treat disease states from the story activity of (II) or to treat disease states from the story activity of (II) or to treat disease states from the story activity of (II) and the production of the detection of (II). (II) is useful for generating antibodies against it detection a grantitating a polypeptide in tissue, as molecular weight markets and is activity of states broadly and the binding partners are useful in activity and absorders involving aberrant procedure activity activities and solutions and activity aberrant procedure activity activities.
 31-MAR-2000; 2000US-0540217
2--AUG-2000; 2000US-0649167
 L _00175067-A2
 minar; chromosome mapping; gene mapping; gene therap;; foreisla;
fusa supplement; medical imaging; diagnostic; genetic disorder;
 wirel human diagnostic protein #13930
 AbGliy39 standard; Protein;
 the polypeptide and polynucleotide sequences have applications in disynostics, forensics, gene mapping, identification of matterns responsible for genetic disorders or other traits to assess chaliconstructed to produce other types of data and products dependent and its analysis and produce agreements. The standard or of sequences ABG00010-ABG30377 represent model toward diagnostic amino acid sequences of the invention.
 New isolated polynucleotide and encoded polygeptides, asetal in diagnostics, forensics, gene mapping, identification of matations responsible for genetic disorders or other traits and to assess busineersity.
 N FSDB; AAS78126
 brinanac RT, Liu C,
 20-MAR-2001; 2001WO-US08631
 11-WCT-2001
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 1s-FEB-2002
 note: The sequence data for this patent did not appear in the princed specification, but was obtained in electronic format directly from William titp.wipo.int/pub/published_pot_sequences.
 Ciaim 20;
 (HYSE-) HYSEQ INC
 :
 359 TATAAATCCTTAGAAAAGAGCATCCCC
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 GlnAlaLysValSerSerMetMetLeuProLeuGlnGlyAlaGinMet. a.GitMetLet.iv.
 GluLysSerLeuArgLysSerLeuPro
 2001-639362/73
 SEQ ID No 44298; 103pp; English.
 (first entry)
6.83
64.00
54.00%
30.00%
 217
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 Length:
Matches:
Conservative:
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 writ 1992-15.00=/16
 20-SEF-199:
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 Micant Chermistable DNA polymerase enzyme MBT-IDE 285
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 255 PITOLE BASS SAAAGAAG TIJAAGIS TIAC 294
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 79 Valle irgsülyfreksniyiValüysfhe ös
 42 ValAinlicSerArgVal------ArgMetSerAlaValCysValLeuArgfnrTrp
 SerAraAstAiaGlyGlnLeuilePysPheThrValPheGlnProCysSerAstValHis
 STITUREL CONTRORGER. LA SCHAL DAGRARCOTHICCATIGOCATA DIGRERACION LES
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 "residios 2-284 deleted from sequence"
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 5-09-762-027-4 (1-388) x AAR23174 (1-609)
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 28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
 Sequence
 See also AAR23140-79 and AAR23722.
 Mutant thermostable DNA polymerase enzyme MET-THR 204 TAF.
 AAR23173 standard;
 Misc-difference
 Thermosipho
 5'-3'; exonuclease;
 22-0CT-1592
 16-APR-1992
 W05206200-A
 9.
10.
10.
 260
 30-SEP-1991;
 140
(CEIU) CETUS
 359 CATCCCC 365
 267 ThrGlnValAlaTyrIleLeuPheGluLysLeuAsnlle-------
 242 TyrGlnGluLysMetAspGlyIleLysGluLysValPheGluIleAlaGlyGlu.....
 60 TGGTTTAATCTACAGGAACCCATAACTTCCTGAAGGTTTATGCTTAACAGTGACAACGG
 20 TATTCTCAGTCCTCCTGGTCTACAAAGCCTGTGATTTCTTGTGTAIGGACAJAACJ:
 eAlaLysLeuLeuGluTyrArgLysTyrGlnLysLeuLysSerThrTyrileAspSe
 ATCATCTTCIFGAGGGAAAGAAGCTGAAGTGCTACATAAGATGCFIGIGCTTCAFAACTC
 AGTCAGTTGAATTTTATTGTGTTTCAGTCCGTAGAGTATTAGCTAACAGAAACCTTTCCA
 rIlePro
 TCAGAAGCTGCAGATTCTGTATAAATCCTTAGAAAAG--
 AlaProTyr-LysLysThrAlaThrGlyLysPheSerThr--
 africanus
 (first entry)
 AA;
 CORP
 90US-0590213.
90US-0590466.
90US-0590490.
 91WO-US07035
 /note- "residues 2-203 deleted from sequence"
 Location/Qualifiers
 9.73
64.00
38.218
23.588
9.748
 -----AsnAlaGluValLeuGluGluLeuSerLysGluHisGluI: 366
 Protein;
 PCR;
 -----ThrPheAsnLeuAsnSerSer----
 amplification;
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 Matches:
Conservative:
Mismatches:
Indels:
 Gaps:
 SSR
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 199
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AARZ3172
AARZ3
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 US-09-762-027-4 (1-386) X AAR2:173 (1-690)
 East Local Similarity:
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 Wil Match
 The sepectic is that all anniunt of thermostable africants polymerase softwity than the native onlyme. Thermostable DNA polymerases are usekn in many recontinuate DNA techniques, espi nucleic acid amplification by the self-sustained sequence replication (SSR) and high temp. ENA sequencing. The absence of 5°-3′ nuclease activity and high temp. ENA sequencing. The absence of 5°-3′ nuclease activity may reconstructe binner sensitivity alletic discrimination in a combined polymerase flyase shain reaction (PECR) assay. An enhanced amt. of 5°-3′ exchiclease activity may be desirable in enzymes used in nonegeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the uniques can be used to prepare a range of recombinant proteins having 5°-3′ exchibites acid to prepare a range of recombinant acriticis.
 Claim II; Page 50: loftp challst.
 inermostatie bik porpositives with artered 51.37 excludibase activity - having object of regions mulated or dereted, for in e.g. Pirk separating and actention assays
 WPI: 1992-150085/LT.
W-PSCS: AAL24333.
 AAR23172 Standard;
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(5)
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 374
 260 AICAICIICTIGAGGGAAAGAAGIGGIGGIACATAAGAIGCTIGIGGIICAIAACIC 319
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 323 lyraladluLysMetAspGl; HeLysGluLysValPheGluTleAlaGlyGlu----- 340
 3 to 7
 361 Alap.dy:-Lystysthra.athr@lytysPheSerthr------
 Ç.
 20 FATIVICAGICCIDETCIGG, HACAAAGCETGIGAFFFCTIGTCTATGGACAGAACGIC
 ASICASITGAATITTATIGISTITCAGTCCGTAGAGTATTAGCTAACAGAAAACSITTCCA 199
 ThrolmValAlaigrIleLedene3luLysLeuAsmile-----------
 TGG111AATCTAJAGGAACCOATAACTTCCTGAAGGTTATGCTTAACAGTGAGAACGTG 139
 chlaf;sleufcanenGlaf_rhrglysfynGlaflysleulysSerfhriyfflehspse
 TIGCCATACTGAGAAACTGGTA MAGGCAGIGTGCCTACAGGTCTACAAAGAAACTICAG 25%
 'A10000 365
 AAA2314c-79 and JAFL5722
 FAG DE
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 -AstalaGluValLeuGluGluLeuSerL/sGluHisGluIl 387
 ------IhrPheAsnLeuAsnSerSet-----
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 rength:
Matches:
Conservative:
Mismatches:
Indels:
 exo nuclésse
 75
 350
 350
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AAR23172:

22-OCT-1992

(first entry)

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Resect Similarity:
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 C
 15-09-762-027-4 (1-388) x AAR23172 (1-754)
 28-SEP-1990;
28-SEP-1990;
28-SEP-1990;
 The sequence is that of a mutant of Thermosipho africanus polymerase mutant designated MET-GLU 140 Tar. having a different ant. of 5-3 exonuclease activity than the native enzyme. However the residue present in the given sequence at position 140 is an Asp. Thermostable DNA polymerases are useful in many recombinant ENA techniques, esp. nucleic acid amplification by PCR, self-sustained sequence replication (SSR) and high temp. DNA sequencing. The absence of 5-3 nuclease activity may facilitate higher assistivity allelic
 Thermostable DNA polymerases with altered 5'-3' exo nuclease activity - having conserved regions mutated or deleted, for use in e.g. PCR, sequencing and detection assays
 Misc-difference
 Thermosipho
 5'-3'; exonuclease; PCR; amplification; SSR; sequencing; PLCR.
 Mutant thermostable DNA polymerase enzyme MET-GLU 140 TAF
 destrable in enzymes used in homogeneous assays for the amplification and detection of a target nucleic acid sequence. Mutation of the DNA encoding particular regions of the enzymes can be used to pregare a range of recombinant proteins having 5'-3' exonuclease activity to a
 30-SEP-1991;
 16-APR-1992
 WO9206200-A
 discrimination in a combined polymerase ligase chain reaction (PLCR) assay. An enhanced amt. of 5'-3' exonuclease activity may be
 Claim 11; Page 59; 185pp; English.
 N-PSDB; AAQ24332
 WPI; 1992-150885/18
 Abramson RD,
 (CEIU) CETUS
 Sequence
 complete
 No . .
 405
 387 TyrGlnGluLysMetAspGlyIleLysGluLysValPheGluIleAlaGlyGlu-----
 86 TGGTTTAATCTACAGGAACCCATAACTTCCTGAAGCTTTATGCTTAACAGTGACAACGTG 139
 20
 also
 TATTCTCAGTCCTCCTGGTCTACAAAGCCTGTGATTTCTTGTCTATGGACAGAACGTC
 lack of activity. AAR23140-79 and AAR23722
 Gelfand DH;
 CORP.
 90US-0590213.
90US-0590466.
90US-0590490.
 Ã
 91WO-US07035
 Location/Qualifiers 1..2
 /note= "residues 2-139 deleted from the native
 10.5
64.00
38.21%
23.58%
9.74%
 sequence"
-----ThrPheAsnLeuAsnSerSer----
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Caps:
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Hypothetical 34.3 kDa protein.
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RIKEN CDNA Q610008P16 gene).
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EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Homo.
 01-MAR-2002 (TrEMBLrel. 20, Cr. 01-MAR-2002 (TrEMBLrel. 20, La. 01-MAR-2002 (TrEMBLrel. 20, La. Hypothetical 34.3 kDa protein.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakuta Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie : Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., I
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 01-MAY-1959 (TrEMBLrel. 10, Created)
01-MAY-1959 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 25.0 kDa protein.
SPBP8B7.12C.
SCHIZOSaccharomyces pombe (Fission yeast).
Enkaryota: Fungi: Ascomycota: Schizosaccharomycetes:
Schizosaccharomycetales: Schizosaccharomycetese;
Schizosaccharomyces.
 BECK A., Reinhardt R, Lyne M., Rajandream M.A., Barrell Submitted (OCT-1998) to the EMBL/GenBank/CDBJ databases EMBL; AL032684; CAA21797.1; *.
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 Hypothetical protein.
SEQUENCE 220 AA; 24997
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SMART: SM00410: IG_like: 1.
 "tymphoid/heuronal cell sarrace OX2 alycoprotein recognizes a novel receptor on macrophages implicated in the control of their function.": Imaunity 13:233-242(20)).
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[Interpro: 1FR00.599: 14.]
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Brown M.H., Barolay A.K.;
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Miranda A., Mungall C.J., Nunoo J., Pacleb J., Parayas V., Park

Patel S., Phouanenavong S., Man K., Yu C., Lewis S.E., kubin G.
 Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY094733; AAM11086.1; ... 846E5487835CACED CR:51; SEQUENCE 404 AA; 43716 MW; 846E5487835CACED CR:51;
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 Stapleton M., Brokstein P., Hong L., Agbayani A., Carisco J., Champe M., Chavez C., Dorsett V., Dresnek D., Frise E., Ghande M., Gonzalez M., Guarin H., Kronmiller B., Li F., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Parayas V., Park S. Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rulin G.M.
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| P93/43508C152E81 CR064;
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AN MEDILINE-20156006; PubMed-10731132;

AN Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocenne J.D.,

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Brandon R.C., Levis S.E., Richards S., Ashburner M., Henderson S.K.,

RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.K.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Preilier B.L.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos J.L.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos J.L.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Eessley E.M.,

RA Burtis M.Y., Benos P.V., Berman B.P., Bhandari D., Bolshab.C. S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center F., Abinara I.

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center F., Faliana I.

RA Dodson K., Doup L.E., Downes M., Duyan Rocha S., Durk., Theilst. S.M.,

RA Burtis N.L., Harvey D., Heiman T.J., Hernandez J.K., Fleisthan, S.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.H., Glasser K.,

RA Fosler C., Gong F., Gorrell J.H., Gu Z., Guan F., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.K., Hutan J.,

RA Kinnel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Merkulov G., Milshina N.V., Nobarry C., Morris J., Moshreti A.,

RA Mcunt S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.
 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta:
Peerygota; Neopera; Endopterygota; Diptera; Brachyceta: Muscomorpha:
Ephydroidaa; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
 Local Similarity:
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 CG6313 protein.
 Q9VCA6;
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 SEQUENCE FROM N.A.
 150
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 167
 122 ArgAsnIlePhe-----LeuLeuPheAlaLeuProTrpIleLeuIhiFheVul-----
 207 ValTyrSerAlaValAsnIleIleIleLeuTyrThrMetArg
 283 CIGAAGTGCTACATAAGATGCITGIGCTTCAIAACTGTCAGA 324
 13
 73
 CGGAACATATTCTCAGTCCTCCTCTGGTCTACAAAGCCTGTGAIITGIIJIGIAIJGAAA
 Gln11e11eGlyGlyGlyValSerLeuGluLysAlaSerHisLeuSerGryAsuSerAry
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 GluLeuGlnGlyLeuPheTrpHisArgSerThrSerValThrLeuIleProTyrTrpSe:
 -----ValIleGlnHisPheCysIleSerAsnTrpArgAlaIleJlnLe:TyrJi;
 GAACGTCTGGTTTAATCTACAGGAACCCATAACTTCCTGAAGCTTTATGOTTAACAGTGA
 ------AlaSerGlyLeuIleAsnTyrIleArqPheTyrMet-----
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A.A. Amanatides P.G., Scherer S.E., Li P.W., Hoskins E.A., Galle F.F.,
A.A. George R.A., Lewis S.E., Richards S., Ashburther M., Hendersch, S.N.,
A.A. Sutton G.G., Wortman J.R., Yandell M.D., Zhang G., Champe M., Pfeifier S.E.,
A.A. Brandon R.C., Royers Y.-H.C., Blazej R.G., Champe M., Pfeifier S.E.,
A.A. Barlow R.H., Doyle C., Baxter E.G., Helt G., Nelson G.R., Mixlos J.L.d.,
A.A. Ballew R.H., Basu A., Baxendale J., Bayraktaroglu L., beasley E.M.,
A.B. Borkova D., Botchan M.R., Bouck J., Brokstein D., Beliala C.,
A.A. Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A.A. Gary S., Dahlke C., Davenport L.B., Dettier P.,
A.A. Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischamn W.,
A.A. Glodek A., Gong F., Gorrell J.H., Gu Z., Glan P., Harris M.,
A.A. Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
A.A. Hostlin D., Houston K.A., Howland T.J., Wei M.-H., It evands G.,
A.A. Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
A.A. Kimmel B.E., Kodira C.D., Kraft C., Kraviz S., Kulp D., Lii X.,
A.A. Liu X., Matteel B., McIntosh T.C., McLeod M.P., McPharson D.,
A. Mount S.M., Moy N., Murphy B., Murphy L., Muzhy D.M., Helson D.L.,
 MESULT 12
 JS-09-762-027-4 (1-368) x QBWRQ7 (1-4001)
 PRINIS: PRO1415; ANKYRIN
PRINIS: PRO0308; ANTIFREEZEI.
SHARI; SHJ0248; ANK; 25.
SHARI; SHJ0322; KH; 1.
PROSITE: PS50088; ANK_REPEAT; 20.
PROSITE: PS50297; ANK_REP_REGION; 2
PROSITE: PS50297; ANK_REP_LEGION; 2
PROSITE: PS50247; ANK_REP_LEGION; 2
PROSITE: PS50247; ANK_REP_LEGION; 2
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Fram; PF00023; ank; 25
Pram; PF00013; KH-doma
 232 ACACIGCCIGCTGCCAGTTTCTCAGTATGGCAATGGAAAGGIIIC 1bo
 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; insectu;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Miscomurpha;
Ephydroidea; Drosophilidae; Drosophila.
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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 MEDLINE-20196006; PubMed=10731132;
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 Ephydroidea; Dro
NCBI_TaxID*7227;
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 33501 protein.
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 292 AGCACTTCAGCTTCTTTCCCTCAAGAAGATGATCTGAAGTTTCTTTGTAJAJACCTGTAJAC
 SerProSerAlaMetSerProAsnHisAspAspIleArgLysMetProAtgProIle3ly
 PRELIMINARY;
 KH-domain; 1.
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Hismatches:
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25K17-150 ok A44326350.
Beyon M., Köctter v., Homers S., Entlan K.-D.,
Mewes H.W., Major K.F.X. School for U.:
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EMBL; AL049171; CAB38964.1; -
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InterPro; IPR001810; F-box.
Pram; PF00646; F-box; 1.
SMART; SN00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1.
Hypothetical protein.
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SEDI Arabidopsis sequencing project;
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 SEQUENCE FROM N.A. Rose M., Hempel S., E Submitted (MAR-2000)
 O5LN44;
01-OCT-2000
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 Q9LN44
 Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kha Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lec C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Hguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri
 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; iracheog
Spermatophyta; agnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Brooks S.,
 238
 257
 Toriumi M., Vaysberg M.,
Ecker J.R.;
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 291
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 57
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 TGGACAGAA---CGTCTGGTTTAATCTACAGGAACCCATAACTTCCTGAAG-----CTT
 ATAAGATGCTTGTGCTTCATAACTCTCAGAAGC-----TGCAGA 333
 431 AA; 49655
 O (TrEMBLrel.
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 PRELIMINARY;
 ----PheLeuThrLeuThrAsnAspHisCysArg 338
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CLMBL: AND/SBGE: ART9444.1; -

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V SEQUENTE 639 AA: 71309 NM: 872EV5EB4D2EDACA CRC64:
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 Pfan: PF00534: .
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 Selomii Sedwawe foi Arabidopsis thallana
| * |
 Eukaryota; Virliplantae: Streptophyta; Embryophyta; Iracheophyta;
spermatuphyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC ol
Panicoldeae; Antropogonoae; Zea.
NOBI_TaxID=4577;
 01-A03-1998 (IILMBLrel. 07, Created)
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Starch synthase EULL1 (Fragment).
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EmbL, AF0216.; AAN14015.1;
InterPro; IPRowl296; Glycos_transt_i.
 MEDLINE-98169340; PubMed-9501110;
Sac M., Wanat J., Stinard P.S., James M.G.,
"Characterization of dull1, a maize gene co
 Zea mays (Maile)
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 GIC DIEGRATALIA (LAGCIARCAGAAACCTI DUATIGCCATACIGAGAACTGGCAGCAG
 isteuLys ii .dluVal
 AAGTGCTA JATAAGATGCTTGT3CTTCATAACTCTCAGAAGCTGCAGA11CTGTATAAAI
 GCA DIGIGACT ACABGICIACAAABAAACIICAGATCATCIICIIGAGGGAAAGAACTG
 FALLIMINARY:
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 HW:
 PKI;
 6410223B553C515E CR264;
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| US-09-762-027-4 (1-388) x 064924 (1-310)          |                                                                                                                                        |
| cgrelagiti                                        | GCCTGTGATTTCTTGTCTATGGACAGAACGTCJGGTTTAAICTACAGGAACCCAIAA 154                                                                          |
| erAlaSerGlaIle                                    | AlaLeuAspTyrIleGluLeuTyrArySerAlaSetGlnIleValifeIleGlnProThr 242                                                                       |
| CAACGTGAGTCAG                                     | 105 CTTCCTGAAGCTTTATGCTTAACAGTGACAACGTGAGTCAGTTGAATTTTATTGTGTTTC 164                                                                   |
| ::<br>erAspAlaAlaIle                              |                                                                                                                                        |
| CITTCCALLGCCA                                     | AGTCCGTAGAGTATTAGCTAACAGAAACCTTTCCALLGCCATACTGAGAAAATTGGCA 221                                                                         |
| roGlyHisCysCys                                    |                                                                                                                                        |
| SAAACTTCAGATC                                     | GlnValProGlyHisCysCysThrAlaSerLeuserLeu 2"2                                                                                            |
| 273 ValSerSerIleProArgGlyAlaGlnCysAsnPheLauSerSer | rLeuSerLeu<br>AJGJAAAGAA                                                                                                               |
|                                                   | rLeuSerLeu<br>A303AAA3AA                                                                                                               |
|                                                   | rLeuSerLeu<br>A3G3hAhGhA                                                                                                               |
|                                                   | h: Intractive 27.39% Intellections: 1  10 98% Indels: 1  10 027-4 (1-388) x 064924 (1-310)  GCCTGTGATTICTTGTCTATGGACAGAACGTCHGGTTTAALC |

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 Post-processing: Minimum Match U%
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 US-09-762-027-4
657
 January 2, 2003, 15:09:29; Search time 13.5 Seconds
 262574 seqs, 29422922 residues
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 agctgctcaatacggaacat
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Copyright (c) 1993 - 2003
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US-08-458-819-12
US-08-222-617A-13
US-08-222-617A-25
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US-08-327-617A-25
US-08-347-492B-2
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| fi<br>S       | '1<br>•        | 9<br>J        | :. 7          | ,¹            |              |                |               |              | e.7             |              |               |                   |               | ٠              |              |                           |                |               |               | ن<br>ن        |                   |                      | <br>c              | . :                |                | \.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\.\. |              | :           | ::            | :               |              |            |
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| -08-137-117D- | T-US95-13233-1 | -08-918-658-1 | -08-954-668-1 | -08-656-055-1 | -901-015-90- | - 08-895-063-4 | - UB-896-063- | -08-257-029- | US-08-257-029-2 | -08-687-379- | -68-687-379-1 | -09-372-658-      | -09-542-749A- | - 08-854-344C- | T-0395-13233 | - <del>08-918-658-1</del> | - 09-268-140-5 | -08-954-668-1 | -06-656-055-1 | -08-540-406-1 | -09-134-001C      | - Uz - 683 - 743 - 4 | - u6 - 325 - 547 - | - U6 - yy3 - 22a - | - JB-152-757-1 | -08-679-493A-                          | -u8-477-537- | -486-117-   | - vs-472-604- | - UB - 121-704- | -19-547-540A |            |
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## ALIGNMENIS

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RESULT 1

Sequence 2: Appl: action PC/IUS9507171

GENERAL INFORMATION:
APPLICAM: M.J.NEY, J.
APPLICAM: M.J.NEW: Humal Chemokine Beta-12

NUMBER OF SELVENCES: 7
CORRESPONDER: JACKELLA, BYPHE, BAIN, GILFILLAN, ALLESSEE: JACKEL FORM:
STATE: AFBLICATION SELECT STATE

COMMUTER: LAW JERSEY

COMMUTER: LAW PS/2

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COMMUTER: LAW
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 Percent Similarity:
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TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
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 US-09-762-027-4 (1-388) x PCT-US55-07171-2 (1-136)
 Alignment stores:
 RESULT 2
FCI-US95-07171-3
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 Score:
 Sequence 3, Application PC/IUS9507171 GENERAL INFORMATION:
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: None
FILING DATE: None
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: 3258
TELECCHMUNICATION INFORMATION:
 SOFTWARE: WORD PERFECT CORRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
 TILLE OF INVENTION: Human Chemokine Beta-12
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
 APPLICANT:
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 LENGIH:
 COUNTRY:
 STATE:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
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 65 ArgLeuValValGlyTyrArgLysAlaLeuAsnCysHisLeuProAlaIleilePheVai 64
 45
 S
 APPLICATION NUMBER: PRILING DATE: 6 JUN 95 CLASSIFICATION:
 OPERATING SYSTEM:
 COMPUTER:
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 ROSELAND
: NEW JERSEY
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 USA
 MOONEY, J.
 SYSTEM: MS-DOS
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 Gelfand, Davin H.
ALLANSON, Richard L.
AVENTON: 5' to 3' LENDUCLEASE MUTATIONS
EVENTON: THEEN STABLE DNA POLYMERASES
SEQUENCES: 38
 MIN AND
 TOWN RUMBER: US 550,450
Ald: 28-SEP-1990
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 11277
. ICN NUMBER:
 App.ication US/07977134
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 ah (AshAryd) uValdysThrAshPro
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 DATATION DATA:
 TPE: Floppy
 ENDE ADDRESS:
 pValAs61hrProSerihrCysCysLeuLysTyrTyrGluLysValLeuProArg
 .Sertewing Stear (1875) Steam (1886) Steam (
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 ICAILON DATA:
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PELTATION DATA:
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 s: Horimann-La Poche Inc.
545 Kingsland Street
 : NUMBER:
 : FR./FEIN
 Macintosh
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 28-SEP-1990
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US 520,394
 Length:
Matches:
Conservative:
Mismatches:
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 Percent Similarity:
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APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 814-2972
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 ATTORNEY/AGENT INFORMATION:
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 NAME: Luann Cserr
REGISTRATION NUMBER: 31,822
 APPLICATION NUMBER: FILING DATE: 02-NO
 APPLICATION NUMBER: FILING DATE: 20-SE
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 ATCATCTTCTTGAGGGAAAGAAGCTGAAAGTGCTACATAAGATGCTTGTGCIICATAACIC ily
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21-DEC-1990
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 sequence 12, Appliaction US/ud158819 Patent No. 5795742
 GENERAL IN-JAMALI
 COMPUTER REALABLE FORM: MEDIUM TYPE: floppy disk
 NUMBER OF SE UZH LES:
CORRESPONDENCE ADDRES
 APPLICANT: ACTAISSO, Pichard D.
HITLE OF INVENTIAL S' TO 3' EX NUCLEASE MUTATIONS
HITLE OF INVENTIAL THERMOSTABLE DAN POLYMERASES
 APPLICATION NUMBER: US 0c3.50v
FILING DATE: 17-JON 1967
PRIOR APPLICATION DATA:
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 PRICE APPLICATION DATA:
 APPLICATION NUMBER: US 8: FILING DATE: 22-AUG-1986 PRIOR APPLICATION DATA:
 FILING DAIE: 12-JAN-
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 PRIOR APPLICATION DATA:
 PRICE APPLICATE A DATA:
 OPERATING SYSTEM: 7
SUFTWARE: WORDPERFECT
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 PRIOR APPLICATION DATA:
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 APPLICATION NUMBER: US 1
FILING DATE: 12-JAN-1988
 APPLICATION NUMBER: US 609,157 FILING DATE: 02-NOV-1990
 APPLICATION NUMBER: US 41 FILING DATE: 22-DEC-1989
 APPLICATI O NUMBER:
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 APPLICATI W W MABER:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
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 15-MAY-1990
 23-FEB-1993
 20-SEP-1990
 26-SEP-1990
 21-DEC-1950
 28-SEP-1990
 20-SEP-1556
 ນຮ 590,213
 US 590,465
 US 746,121
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 US 455,611
 US 585,471
 WO PC1/HS50/u7641
 US 899,241
 US 523,394
 US 530,490
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best Local Similarity:
 Alignment Scores:
 : MOLECULE TYPE: protein
US-08-458-819-12
 TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 12:
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REFERENCE/DOCKET NUMBER: Ca-
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
 SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
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 NAMACTERISTICS:
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L.E: 15-AUG-1991
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 https://documents.com/documents
 S NUMBER: US 000,500
.E: 17-JUN-1987
 H NAMEER:
 N N MBER: POI/USTI/ TOUS
 ENTERIOR DE LE CONTROL DE L'ANTION DE L'AN
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 A GUMBER:
 H GUMBER: 32,630
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 15-MAY-1990
 48-SEF-1954
 2d-SEP-1999
 22-AUG-1586
 12-JAN-1988
 28-SEP-1990
 1-JUL-1950
 A DATA:
 1. 95
64. 50
38. 218
23. 588
 US 555,241
 US 14:.441
 US 523, 334
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 Case No.
 Matches:
Conservative:
Mismatches:
Indels:
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 Sequence 13, Application US/08222617A
Patent No. 5882879
 REFERENCE/DOCKET NUMBER: 9
INFORMATION FOR SEQ ID NO: 13:
 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
 APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
 HOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO
 SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
 SUFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 APPLICANT:
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 APPLICATION NUMBER: US/OFFILING DATE: 04-APR-1994 CLASSIFICATION: 435
LOCATION: 1..3665
OTHER INFORMATION:
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 INFORMATION:
 Chicago
 60606
 Illinois
 E: McDonnell Boehnen Hulbert & berghoff
300 South Wacker Drive
 3665 amino acids
 USA
 Gutierrez, Santiago
 Martin, Juan F.
Garcia, Bruno D.
 Palissa, Harriet
 Von Doehren, Hans
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 Veenstra, Annemarie
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 US/08/222,617A
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 /label= ACVS
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IIILE d INVITAL AB: Quantitles of ACV Synthetase
NUMBER F SEJURNES: 27
CORRES: NUENCE AUDRESS:
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 2158 At the physician 2152
 2114 Alastovás AlaTipSétis pAspVaiPherrrrrrrrrrrrrrrrrrrrrrrrGln 2124
 2094 ij: 110...Varargas; 1:yaryThrLeuSerPheAlaSerHeValCysHisHisLeu 2113
 2074 Br. Dr.S. C.n.Brahlsbrachetystenbap3InGluLeubroflehisValArgLeu 2093
 2055 To The Schröding Valoria Short SeraluThrGluMet---GlodiyargMet
 APPLICANCE
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/222.617A
 APPLICAN:
 APPLICAGE:
 STAIL: CLIMA
 214 --- 10 TADIA/GREAT GRANDUTTICI GITAGCTAA/ACICIAGGACIGAAACAC 158
 298 HALDLA TATLEMADILITERCOPARDANAMICHOARGHIT ...
 157 ANIANNEL MALIGACI A MITGICACIMITAAGCATAAAGCIICAGGAAGTTATGGG 98
 97 Tr 1131.
 37 AJAJJATTVI, JAJA 28
 ADDRESSEE: McConnell bechner Hulbert & Berghoff STREE: A South Warker Drive
 COUNTRY
 ZIP: Euter
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Eest Local Similarity:
 RESULT 8
US-08-222-617A-25
 JS-U$-762-027-4 (1-388) x US-08-222-617A-4 (1-3712)
 Query Match:
 score:
 Alignment Scores:
 US-08-222-617A-4
 Sequence 25, Application US/08222617A Patent No. 5882879 GENERAL INFORMATION:
 APPLICANT: Veenstra, Annemarie E
APPLICANT: Martin, Juan E.
APPLICANT: Garcia, Bruno D.
APPLICANT: Gutierrez, Santiago
APPLICANT: Barredo, Jose L.
AFPLICANT: Von Doehren, Hans
APPLICANT: Palissa, Harriet
Palissa, Harriet
 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGIH: 3712 amino acids
 FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
IIILE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolati
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
 2158 AryArgAlaLeuArg
 2125 ArgAspLeuAspAlaPheTyrAlaValHisThrLysHisLysAlaAlaAlaAlaAssLed---
 2114 AlaPheAspAlaTrpSerTrpAspValPhe-----
 2094 TyrGlnValValArgAspGlyArgThrLeuSerPheAlaSerlleValCysHisHisHsLea 2113
 2074 AlaGluSerThrAlaHisAlaPheLysLeuAspGluGluLeuProIleHisValArgLeu 20+5
 2055 LeuPheSerValAspValLeuArgLeuThrSerGluThrGluMet - - - 31:Gl; ArgMet
 FEATURE:
 MCLECULE TYPE: protein
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 157
 298 TIATGTAGCACTTCAGCTTCTTTCCCTCAAGAAGAIGATCTGAAGTII-------
 358 CICITTICTAAGGATITATACAGAATCTGCAGCIICIGAGAGIIAIGAAGCACAAGCAI
 OTHER INFORMATION:
 37 AGAGGAGGACTGAGA
 97 TICCIGTAGATTAAACCAGACGTTCTGTCCATAGACAAGAAATCACAGGCTTTGTAGACC
 NAME/KEY: Modified-site LOCATION: 2555
 FOPOLOGY:
 REFERENCE/DOCKET NUMBER:
 ---TICTCAGTATGGCAATGGAAAGGTTTCTGTLAGGTAATACTCTAGGJAGTJAAATAG 156
 AAIAAAATTCAACTGACTCACGTTGTCACTGITAAGCAIAAAGCITCAGGAAGIIAIGGG 98
 ----CTTTGTAGACCTGTAGGCACACTGCCTGCIGCCAGI----
 amino acid
 linear
 3.05
64.00
37.60%
24.80%
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 --ProThrLenAryValGluTyrLysGluTyrAlalicSiuHis 215
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 Percent Similarity:
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US-08-347-4928-2
 ŪS-∪9-762-0∠7-4 (1-388) × ∂S-Ū5-222-617A-25 (1-3712)
 whery Match:
 7100
 Aliquient Source:
 TOPOLOGY:
#OLECOLE TYP
#3--08-222-817A-28
 Sequence 2, Apprication US/Uss474926
Patent No. 5602708
GENERAL INFORMATION:
 INFORMATION (SEE TO NO): 2
SEQUENCE: "MAYATEFISICS:
LENGTH: STIT SAILS SCIUS
TYPE: dails acid
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Referenta/Lighei mumber:
 MEDION TIPE: Frippidisk
COMPUTER: IBM E-Tompathle
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SOFTWARD PRICED IN POLOZYMS-1 OF VERSION
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 2024 ljiGlivalVatAryAspOlyArgInrLeuSerPheAlaSerIleValCjsHisHisLeu
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 2055 LeukheSerValhapVallenArgLeuThrSerGluThrGluMet---GlnGlyArgMet
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 298 TIAIGIAGUMUIFEMBOIICHITCOOLGAAGAAGATGATCTGAAGHII--
 358 CICLITICIAAGJAITIATACAGAAICIGCAGCITCTGAGAGITATGAAGCACAAGCATC
 TIP: 600 P 13 TO AND THE PART MOTORM.
 FRESPONDENCE AND PESS:
ALDRESSEE: Modernel Buennen Hutbert
STREET: 3-0 SOLLE Wacker Little
CITY: Chicago
STAIE: Hilloris
COUNTRY: 0-88
 FILING FATE: 04 AFR
 CLASSIFICATION:
 o7 Adaddad ACT Jala
 A. TASPLEGASPA: aPreTyrAlaValHISTLrLySHISLySAldAldAldAsrLed***
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 AlaGluSerInrAlaHisAlaPheLysLeuAsp3luGluLeuProffeHisValArgLev 2093
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 Wilder Craig G
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 Matches:
Conservative:
Mismatches:
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APPLICANT: APPLICANI:

Scilliamer, Jeffrey J.

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 K
 US-09-762-027-4 (1-388) x US-08-347-4928-2 (1-120)
 query Match:
 Percent Similarity:
Best Local Similarity:
 ** Patent No. 5936068
GENERAL INFORMATION:
 US-08-798-143-2
 Pred. No.:
 Alignment Scores:
 KESULT 10
 APPLICATION NUMBER: US/08/347,4928
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA: 08/303,241
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
 TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 IMMEDIATE SOURCE:
LIBRARY: LIVER
CLONE: 87825
 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals, Inc
 TITLE OF INVENTION: FITLE OF INVENTION: NUMBER OF SEQUENCES:
 COMPUTER READABLE FORM:
 TELEPHONE: 415-855-0555
 APPLICANT:
 APPLICANT:
 APPLICANT:
 MOLECULE TYPE:
 214 AACTGGCAGCAGGCAGTGTGCCTACAGGTCTAC---AAAGAAACIICAGAICATCTICC 27
 STREET: 3174 POI
CITY: Palo Alto
STATE: CA
 271 GAGGGA-----AAGAAGCTGAAGTGCTACATAAGATGCTTGTGCTTCETAHCTGTCAJA 5-4
 REFERENCE/DOCKET NUMBER: PF-0024
 COUNTRY: U
ZIP: 94304
 NAME: Luther, Barbara REGISTRATION NUMBER:
 MEDIUM TYPE:
 32 AsnThrProSerThrCysCysLeuLysTyrTyrOluLysValLeuFroArgArgLeival 5:
 72
 52 ValGlyTyrArgLysAlaLeuAsnCysHisLeuProAlaLleflebheValantLyskrg
 SIRANDEDNESS:
 TOPOLOGY:
 LENGTH:
 AsnArgGluValCysThrAsnPro 79
 AGCTGCAGATTCTGTATAAATCCT 348
 amino acid
 Application US/08798143
 3174 Porter Drive
 120 amino acids
 U.S.
 LIVER
Wilde, Craig G.
Hawkins, Phillip R.
Bandman, Olga
Seilhamer, Jeffrey J.
 linear
 Diskette
 peptide
 single
 1.23
63.50
47.92%
33.33%
9.67%
 EXPRESSED CHEMOKINES PRODUCTION AND USES
 Indels:
 Conservative:
 Mismatches:
 Matches
 Length:
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Percent Similarity:
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FCI-USy5-151di
 53-∂y-762-62°6 (1-3dd) x US-68-7yd-143-2 (1-126)
 Allghment Sculvs:
 Sequence 2 Application PC/IUS9515484
SENERAL HS RMATION:
ALPLICARS: IN-YIE PHARMACEUTICALS
 IELEFAN: 415-6
INFURMATILN FUR SF
 NUMBER : SEQUENTES:
CCHREST. N. ENCE ALCRESS
AUDRESSEE: IL 7, LE PI
 PRIOR AFFICIAL NUMBER: 08/34/
FILIN: AFE: 29-NJV-1994
AFFICIALIDA NUMBER: 08/30/3
 SCETWARD: FUSISEQ Version 1.5
CUPREM, APPLICATION DATA:
 CCMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
CCMPUTER: IBM COmpat
 REFEREN'E/DUCKLI NUMBER: PF
TELECORRUGICATION: INFORMATION:
TELEPH No. 1415-855-0555
 APPLICATION ROWSER: 08/3 FILING LATE: F-CCT-1994 ATTORNEY/AJENT TO RMATION:
 M LECULE TYPE: populde IMMEDIATE SHURCE.
 PRIDE AF: ICATI'N DAIA:
 SECUENCE CHARACTERISTICS:
AFFLICANT: INTYLE PHARMACEUTICALS, 180.
TILLE (F. NVENTICA): EXPRESSED CHEMOKINES, THEIR PROJUCTION AND
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 TENGIH:
 NAME:
 214 AACT GIAGONIGIAGIGOGIAGAGITCIAC---AAAGAAACIICAGAIGATCIICII 270
 APPLICATION WORBER: FILING LATER
 325 AGT: CAGAITCIGIATAAAFCCI 348
 27) GA 113A-----AAGAAGTIGAAGIGCIACAIAAGATGCITGTGTGTAIAACIGTGAJA 324
 CLONE
 CLASSI: .
 OPERATING SYSTEM:
 52 Vari., TyraratysalateuAsnCysHisteuProAlaIleIlePheValThrtysArg 71
 32 As....broSerinrCysCystentyStyrTyrGtulysValteuProAcgAcgLouVal 51
 LIBRALIT
 STRANGE WESS:
 NAME: ...ther, Barbara
REGISIFATION NUMBER: 3
 72 AsiA: GluVal ysthrAsnPro 79
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 ID NO: 2:
 1.28
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47.626
33.338
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 00/303,211
 US/v8/790.145
 08/320,011
 33,954
 PF-0024
 Indels:
Gaps:
 Mismatches:
 Matches:
Conservative:
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TITLE OF INVENTION: NUMBER OF SEQUENCES:

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 US-09-762-027-4 (1-388) x PCT-US95-15484-2 (1-120)
 Percent Similarity:
Best Local Similarity:
 CLUNE: 87825
PCI-US95-15484-2
 RESULT 12
 Query Match:
 Alignment Scores:
 US-08-720-258-2
 Sequence 2, Application US/08720258 Patent No. 5871740
 GENERAL INFORMATION:
 TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CORRESPONDENCE ADDRESS
 APPLICANT: Smith, Craig A.
ITILE OF INVENTION: Chemokine Inhibitor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
 NO.:
 IMMEDIATE SOURCE:
 MOLECULE TYPE:
 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
 CLASSIFICATION:
AITORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, Version #1.50
 214 AACTGGCAGCAGGCAGTGTGCCTACAGGTCTAC---AAAGAAAJTTCAGAAJATGTI'II 27
 LIBRARY:
CLONE: 8
 STREET: 3174 POI
CITY: PALO ALTO
STATE: CA
 325
 271 GAGGGA-----AAGAAGCTGAAGTGCTACATAAGATGCITGIGGITGAIAAGTGIGASA 324
 APPLICATION NUMBER: US 0 FILING DATE: 29-NOV-1994
 APPLICATION NUMBER: FILING DATE: 29-NOV CLASSIFICATION:
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N
 TYPE: amino acid
STRANDEDNESS: si
 NAME: LUTHER, BARBARA REGISIKATION NUMBER:
 52 ValGlyTyrArgLysAlaLeuAsnCysHisLeuProAlailellePheValinrLysArg 71
 LENGTH:
 72 AsnArgGluValCysThrAsnPro 79
 IOPOLGGY:
 AsnThrProSerThrCysCysLeuLysTyrTyrGluLysValLcuProAigArgLeuVar 51
 AGCTGCAGATTCTGTATAAATCCT 348
 94304
 E: INCYTE PHARMACEUTICALS, IN...
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 120 amino acids
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Immunex Corporation
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 peptide
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9.67%
 US 08/347,452
 PCT/US95/15484
 33954
 PF-0024 PCT
 Length:
Matches:
 Gaps:
 Mismatches:
Indels:
 Conservative:
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Percent Similarity:
Best Local Similarity:
 Fred. No.:
 Alignment Scores:
 38-19-702-127-4 (1-388) X US-18-720-258-2 (1-246)
 APPLICAMI ISHI, YOSHITAMI APPLICAMI KOMISHI JIL APPLICAMI KOMISHI JIL APPLICAMI KOMISHI JIL APPLICAMI HIYSSAMA KATAMI APPLICAMI MASAMA HIMON APPLICAMI SAZUKI, MASAMAH APPLICAMI SAZUKI, MASAMAH APPLICAMI SENSE IN JUNIO DESULFURIZATION ENZYMES FILE REPREBULL 1128 - ODINI DESULFURIZATION ENZYMES CURRENT APPLICATION HUMBER: US/MY/17.54vA CURRENT FILES DATE: 2000-1-5-29
 GENERAL THE JRMATION:
 Sequence o, Applisation Us/occ4754vA
Patent No. 6420158
 INF AMAII OF FOR SEV ID NO. SE_OBNOE CHARACTERISTICS: LENGTH: 249 amino acids
PRIOR APPLICATION NUMBER: JF 310545/1998
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: JF 090387/1998
 PRIOR APPLICATION NUMBER: POT/JP99/01756
PPICR FILING DATE: 1955-04-02
 TELEPHONE: (206) 587-5430
 PRI R APPLICATION DATA:
APPLICATION NUMBER: US A
PILLIA DATE: 29-SEP-19-5
ATT ANEY/AGENT INFORMATE A:
 PFILE APPLICATION DATA:
APPLICATION NUMBER:
FILING LATE: 20-DEC-
 : MPULER READABLE FORM:
 MEDIUM 1998: Floppy disk
MEDIUM 1998: Repet Macintush
PERATINA SYSTEM: Apple System 7.5
S.E.WARE: Microsoft W.dd, Version
1998: APPLICATION DATA:
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 TELEFAX: (LL)
 RESISTRATION NUMBER:
 APPLICATION NUMBER:
ELLING DATE: 26-SE
LLASSIFICATION: 43
 REFERENCE/DOCKET NUMBER: Liter-B
 F.A.E: Washington
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 Andersch, Kathrib A.
KATTON NUMBER: 5-172
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 5. C.1. C. . . .
 (206) 233-1644
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 protein
 UMBER: US .8/575.715
20-DEC-1535
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 3.49
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51.728
 4.200
 05/v8/720.25e
 10/537.324
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 Length:
Matches:
Conservative:
 Gaps:
 Mismatches:
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 Percent Similarity:
Best Local Similarity:
 LENGIH: 432
TYPE: PRT
ORGANISM: Paenibacillus sp.
US-09-647-540A-8
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 US-09-762-027-4 (1-388) x US-09-647-540A-8 (1-432)
 Pred. No.:
 Alignment Scores:
 Query Match:
 : TYPE: PRT ; ORGANISM: Paenibacillus US-09-647-540A-9
 US-09-647-540A-9
US-09-762-027-4 (1-388) x US-09-647-540A-9 (1-432)
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 Percent Similarity:
Best Local Similarity:
 Pred. No.:
 Alignment Scores:
 PRIOR FILING DATE: 1998-04-02
NUMBER OF SEC ID NOS: 21
SOFTWARE: FRASTSEC for Windows Version 4.0
SEC ID NO 8
 Sequence 9, Application US/09647540A Patent No. 6420158
 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9
 GENERAL INFORMATION:
 PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 310545/1598
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: JP 090387/1998
PRIOR FILING DATE: 1998-04-02
 CURRENT APPLICATION NUMBER: US/09/647,540A CURRENT FILING DATE: 2000-09-29 PRIOR APPLICATION NUMBER: PCT/JP99/01756
 APPLICANT: Suzuki, Masanori
TITLE OF INVENTION: GENES ENCODING DESULFURIZATION ENZYMES
FILE REFERENCE: 11283-006001
 APPLICANT: Ishii, Yoshitaka
APPLICANT: Konishi, Jin
APPLICANT: Hirasawa, Kazuaki
APPLICANT: Okada, Hideki
 NUMBER OF SEQ ID NOS:
 LENGTH: 432
 220 CAGCAGGCA 228
 160 GTTTCAGTCCGTAGAGTATTAGCTAACAGAAACCTTTCCATTGCCATACTGAGAAACTGG
 100 CATAACTTCCTGAAGCTTTATGCTTAACAGTGACAACGTGAGTCAGTTGAAIITTATIGI 15:
 130 ProLysAla 132
 4.5
 40 TCTACAAAGCCTGTGATTTCTTGTCTATGGACAGAACGTCTGGTITAATCTAGAGGAACC
 His---PheAlaGluLeuLeuAla------GluHisGluAsnTleHisLeuSerVal löv
 4.17
61.00
47.628
34.928
9.288
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61.00
47.62%
34.92%
9.28%
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 Mismatches:
Indels:
 Conservative:
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 Length:
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 US-08-329-704-2
 Percent Similarity:
Best Local Similarity:
Query Match:
 ; Sequence 2, Applic
; Patent No. 5786210
 # 15:00LE TYPE:
US-ud-329-764-2
 SCOTE:
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 GENERAL INFORMATION:
 IN AMAILWAY A 15-4 25-12-0
STEWNS CHARACTERISTUS:
SERVICE THA BOLLD A 16-12
TANCO
 HEFERENCE/DOCKE, NOMBER: IA.
IT.LECOMMONICATION THE FRATERY
TELEPHANE 415-452-156
TELEPHAN: 415-476-1207
 MEDIUM TYPE: FLOPPy disk
CLMPUIER: IBM PC COMPARINE
PERAITHO SYSTEM: PC-DOS/MS-DOS
S ETWARE: Patentin Release *1.0, Version *1.25
CLFRENT APPLICATI'N DAIA:
 APPLICANT: Kennery, Jucquelling L. APPLICANT: Zlotnik, Albert
 APPLICATION NUMBER: US 00/1/3/483 FILING DATE: 00*FEB*1994 FALSE APPLICATION DATA:
 CIRRESPUNDENCE ALGRESS:
 APPLICATION NUMBER: US UM/
FILING DATE: 22-APR-1594
ATT: RNEY/AGENT INFORMATION:
KAME: Ching, Elwin P.
KESIS: RATION NUMBER: 34,00
 APPLICAMI: Kelner, Gregory
 io - Probyskia lisa
 FOR GITTOAGTOCGTAGAGTATTAGCTEANDAGAAGCTTTCCATTGCCATACTGAGAAAGTGG
 LES CAUCAGOSSA 214
 SIREET: 901 Car
DITY: Palo Alto
STATE: Californ
 APPLICATION NUMBER: US/O
 ADDRESSEE:
 THE OF INVENTIONS:
 TYPE:
 LASSIFICATION: 436
 P. Town
 DOLADAMA PODI DI BATITOTI BI DIATBBADA BAACGTOTGGTTTAATOTACAGGAACO
 His---Phealultaleuleuktar
 CALARCIE DOTORAS CLITATO VILAR INSTORCAROGIGAGICAGITORATITITATIGI 159
 94304-1164
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 Application US/083297
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 DNAX Research Institute
 p: Jtein
 5.3
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45.07%
28.17%
8.96%
 MARMALIAN THYMUKINE GENES
 US UB/231.421
 US/v8/329.764
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 ····--GluHisGluAsnIleHisLeuSerVal 109
 Mutches:
 Mismatches:
Indels:
 Conservative:
114
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27
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US-J9-751-027-4 (1-388) x US-08-529-704-2 (1-114)

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 fitle:
Terfect score:
 kun on:
 im nucleic - protein search, using frame_plus_n2p model
 Catabase :
 -Q=/Cgn2 1/USFTO_SPOO1/US09762027/runat_02012003_095614_2632/app_qnery.fista_1.533
-DB=Published_Applications_AA -QFMf-fastan -SUFFIX=n2p.rapt -MINMACh+0.1
-DOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX > LOUGHA-0.1
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct -(HR_MAX=10)
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEH-c
-MAXLEN=200000000 -USER=US09762027_2CGN_1_1_2_3Tunat_0201200_3_055614_2662
-NCPU=6 -TCPU=3 -NO_XLPXY -NO_MMAP -LARGEOUERY -NEG_SCORES-0 -GAIT -LPAGLIZ-
DEV_IMBOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=10 -YGAPDXT=0.5 -DELOP=6 -DELEXI=7
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 lotal number of hits satisfying chosen parameters:
 Searched:
 scoring table:
 -MODEL=frame+_n2p.model -DEV*xlh
 Result
 NO.
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
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60
 91
77
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US-09-925-300-1065
US-09-867-550-930
US-09-768-894A-2
US-09-943-798-2
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 Description
 Sequence 930, Ap. Sequence 2, Applia
 Sequence 1065, Ap
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| <br>                  |                 | =                | ::<br>=                | Ξ               |               | <u>ٿ</u> .      | -               | -              | =               | l.               | ς,                | ک               | -               | 7              | ٠.              | ve -              | č         |               | <u>-</u>          |             |           |              | •                | c.          | ٠.              | -           | <u>~</u>        | 7.              | <u>,                                    </u> | <u>.</u>       | Vi.            | -              |                      |                 |                | Ξ,              | :               |                  | *                      | ٠            |
| US-09-925-300-1305    | -801-368-24     | -771-656-2       | -771-956-2             | -771-956-       | -962-646-     | -962-646-4      | -771-956-3      | -771-950-      | - 952-545-5     | -114-454         | -953-956-         | 055-275-2       | ร-เชาช15-348-   | -815-218-      | - 815 - 24a-4   | 514-157-3         | -747-727- | -d15-242-122  | Ū9-815-242-5376   | U-U46-961-7 | 115-195-2 | 9-541-831-17 | U9-771-956-2     | 09-771-956- | 09-898-533-5    | -815-242-49 | -05-815-242-105 | 5-10-052-586-39 | 5-04-949-192-5                               | s-69-870-574-3 | -10-066-566-13 | - Uj-771-956-2 | - 11 - 171 - 156 - 1 | -656-           | -199-305-745-2 | - 956-771-956-2 |                 | US-69-771-956-20 | - v. 3 - 864 - 761 - 4 | 0, 11, 10, 1 |
| Sequence 1305, Ap     | equence 242. Ap | equerice 22, App | equence 24, App        | equence 9, Appl | equence 2, Ap | equence 4, Appl | equence 30, App | equetice 13, A | iddw 'q apparta | equelice s, Appl | Sequence 8, Appli | quence 2, Appli | equence 2, Appl | equence 13, Ap | equens∈ 4, Appl | quence 3, Appli   | 4, App    | equere 12291, | Sequence 5376, Ap | equence 7,  | 2,        | equence 17,  | equerice 27, App | equence 26  | equence 5, Appl | 4523, A     | equence 105     | equence 390, Ap | equence 5, Appl                              | : 3, Appl      | quence 137,    | equetice 25,   | equence 10, App      | equence zl, App | equence zs,    | equence 23, App | equence 6, Appl | nce 20,          | equence 107            |              |

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GENERAL No. ARADION:

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TITLE CE TRYENTIAN MINER: US/NY/925/300

CORRENT ALCIDATIN MUNEL: US/NY/925/300

CORRENT ELLIA TATE: 2001-08-10

PRIOR FILING CATE: 2001-08-10

PRIOR FILING TATE: 1001-08-10

PRIOR FILING TATE: 1001-08-10

PRIOR FILING TATE: 1000-120

STEWARK: PALICALTH MUNEL: 1300-05588

PRIOR FILING TATE: 1000-12

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SEQ ID N. 1005

TYPE: PRI

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Sequence 2, Application US/05768854A

Patent No. US20020115102A1

GENERAL INFORMATION:
AFPLICANT: Diane Joan Cousens
APPLICANT: Steven Michael Foord
APPLICANT: Diane Michael Foord
APPLICANT: Filippo Volpe
ITILE OF INVENTION: NOVEL PROTEIN
FILE REFERENCE: PG3770US
CURRENT APPLICATION NUMBER: US/05/768,854A
CURRENT FILING DATE: 2002-02-24
PRIOR APPLICATION NUMBER: 09/768,854
PRIOR FILING DATE: 2001-01-24
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 US-09-867-550-930
 APPLICANT: Topper, James

TITLE OF INVENTION: No. US20020082206A1el Privinucleotides from Acherogenic IIILE OF INVENTION: Thereby

FILE REFERENCE: 21402-013 (Cura-313)

CURRENT EPLICATION NUMBER: US/9/867,550

CURRENT FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: USSN 60/208,427

PRIOR FILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 2125

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 930

LENGTH: 181

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 APPLICANT: Leach, Martin D
APPLICANT: Mehraban, Fuad
 APPLICANT:
 NUMBER OF SEQ ID NOS: 2
 ORGANISM: Homo sapiens
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Patent No. US20023065 LT
 APPLICANT: Glass Group classes:

IIILE FE INVENTION: 1 (ed. 16)

FILE FERENCE: GST.

CURRENT APPLICATION CONTROL (ed. 2)

CURRENT FILING CALE: 2 (1 - e - s)

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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-08-03
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
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 Percent Similarity:
 Sequence 4, Application US/09943798 Patent No. US20020065215A1
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 GENERAL INFORMATION:
 APPLICANT: Glaxo Group Limited TITLE OF INVENTION: Polypeptide FILE REFERENCE: QG1021
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON HUCLEIC ACID FRUBES TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROAKRAY FILLE REFERENCE: Aeomica-X-1
 APPLICANI: Penn, Sharron G.
APPLICANI: Rank, David R.
APPLICANI: Hanzel, David K
APPLICANI: Chen, Wensheng
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CURRENT FILING DATE: 2001-08-31
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Hanzel, David K.
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Conservative:
 Mismatches:
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 SCUTE:
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LENJIH: 224
 APPLICANT: Founet: Michele
APPLICANT: Brodber W. Wobbin
APPLICANT: Krouse W. Wobbin
APPLICANT: Krouse W. Arimeric Neuropeptide Y Receptors
FILE GF INVESTIGATION: Online OF Neuropeptide Y Receptors
FILE REFERENCE: ALTERNOSION NOVIBER: US/V9/771.955
 PRIOR APPLICATION CUMBER US 60/234,567
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PRIOR APPLICATION COMBER: 05 09/608,406
PRIOR FILING LATE: 20 Y-06-10
PRIOR APPLICATION CAMPER: 05 09/774,205
PRIOR FILING LATE: 2: -01-29
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APPLICANI: beunett, Michele
APPLICANI: Biodbeck, Robbin
APPLICANI: Kianse, James
IIILE OF INVELTION: Chimeric Neuropeptide Y
FILE REFERENCE: N2000.001
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CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 350
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Pred. No.:
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Conservative:
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 1 Sec 11 NO 23
 i sequence 20 Application US/c9771956
 Patent NO. USL (IOVO1474A)
 demend INFORMATION:
 US-09-77
 Percent Similarity:
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 CORRELL APPLITATION HUBBEK: US/09/771,956
TORRERN FILTIG DATE: 2001-01-29
TORRERN SE, ID HOS: 31
STRINGRE: Fatorith Ver. 2.1
 APPI MANI: bennett, Michele
APPL MANI: brusheck, Roboth
APPL Mani: Krause, Jemes
Tills of Invention: chihario Hearopeptide Y Receptors
Till REFERENCE: MIONO.001
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US-09-771-956-21
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LENGTH: 378
 Sequence 21, Application US/09771956 Patent No. US20010031474A1 GENERAL INFORMATION:
 GENERAL INFORMATION:
 Sequence 23, Application US/09909745 Parent No. US20020119546A1
 APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Omolayo O.
IIILE OF INVENTION: Squalene Synthesis Enzymes
FILE REFERENCE: BB1112 US CIP
CURKENT APPLICATION NUMBER: US/09/909,745
CURKENT FILING DATE: 2001-07-20
 PRIOR APPLICATION NUMBER: 60/107,241
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 60/107,241
PRIOR ETILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
 APPLICANT: Bennett, Michele
APPLICANT: Brodbeck, Robbin
APPLICANT: Krause, James
TITLE OF INVENTION: Chimeric Neuropeptide
FILE REFERENCE: N2000.001
CURRENT APPLICATION NUMBER: US/09/771,956
CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
 TYPE: PRT
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 151 CTAATACTCTACGGACTGAAACACAATAAAATTCAACTGACTCACGTTGTCACTGTTAAG
 365 PheThrAlaLeuIleGlyGlyAsnGlyAlaGlnIleCys
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 tProLeuHisValPheHisValValThrAspPheAsnAspAsnLeuTleSerAsnAtj#i >
 TATAAATCCT 348
 GCIGAAGTGCTACATAAGATGCTTGTGC---TTCATAACTCTCAGAAGCIGUAGATI;IJ 215
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 HisLysLeuValSerLysLeuThrGlyAlaGlyGlyGlyGlyCysValLeuInrLeuLeu 343
 sLeuAsnPro 328
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 Mismatches:
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Conservative:
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 APPLICANI. Krause, James
IIIIE of LuckHilon: Chimer: Neuropeptide Y Receptors
File Reference: N2000,001
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CURPERT F...ICA DATE: 2001-01-29
NUMBER OF ST. ID NOS: 31
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 US-09-771-556-25
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 APPLICANT: Bennett, Michel APPLICANT: Brodbeck, Robbi APPLICANT: Krause, James IIILE OF INVENTION: Chimer FILE REFERENCE: N2000.001
 NUMBER OF SEQ ID NOS: 31
SUFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 25
LENGTH: 395
TYPE: PAT
 Sequence 25, Application US/09771956 Patent No. US20010031474A1
 GENERAL INFORMATION:
 CURRENT APPLICATION NUMBER: US/05/771,956
CURRENT FILING DATE: 2001-01-29
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 324 sLeuAsuPro 327
 287
 267
 235 ValCysLeuThrValSer-HisThrSerVal-------CysIleArgLeuL;sans--
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 177 AITAGCTAACAGAAAC------
 117 TTATGCTTAACAGTGACAACGTGAGTCAGTTGAATTTTATTGTGTTTTCAGTCTGTAEAGT
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 ------ArgAsnAsnMetMetAspLysIleAijAspSerLysTyrArqSerSerAr 268
 Bennett, Michele
 ON: Chimeric Neuropeptide Y Receptors N2000.001
 7.56
59.00
41.35%
25.00%
8.98%
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 ----CTTTCCATTGCCALACTG-----AGAAACTGGCA
 Matches:
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Patent No. US2002 .7

GENERAL INFORMATION
 APPLICANI: AVI J.
APPLICANI: Kevin
 APPLICANT:
 PRIOR APPLICATION TO THE PRIOR FILING DATE: 19-7-09-17
PRIOR APPLICATION NUMBER: 6 / PRIOR APPLI
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 PRIOR FILING DATE: 2 1-11-15
PRIOR APPLICATION NUMBER: 60/050974
PRIOR FILING DATE: 1007-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1007-09-17
 TITLE OF INVENTION: SEIRETEL AND IKANSHEMBRANE POLYPEPTIDES AND NOCLEIC TITLE OF TAVENTION: ANIDS ENDOTHS THE SAME
FILE RELEKBLIE: 15.5.5167
CORRENT APPLICATION NAME: 2002-02-01
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 PRIOR APPLICATION NUMBER: 60/079203
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 APPLICANI:
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 APPLICATION NUMBER: 50/056354
FILING DATE: 12.7-11-21
APPLICATION NUMBER: 50/05640
FILING DATE: 12.7-11-25
APPLICATION NUMBER: 50/05654
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APPLICATION MOMENT 60/063329
FILING DAIE: (3-7-10-27
APPLICATION HUMBER: 60/06333)
FILING DAIE: 15-7-10-25
 APPLICATION NUMBER: 6 /462816
FILING DATE: 1597-10-24
 APPLICATION WOMBER: 60/059566
APPLICATION NUMBER: 60/074005
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OR AFFLICATION NUMBER: 60/09598
OR FILING DATE: 1998-08-10
OR AFFLICATION NUMBER: 60/097000
OR FILING DATE: 1998-08-18
OR AFFLICATION NUMBER: 60/099601
OR FILING DATE: 1998-09-09
OR AFFLICATION NUMBER: 60/099803
OR FILING DATE: 1998-09-10
OR AFFLICATION NUMBER: 60/099811
OR FILING DATE: 1998-09-10
OR AFFLICATION NUMBER: 60/099812
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FILING DATE: _ .VI-J1
 APPLICATION Northern POT/USvs/14552
FILING DATE: 1998-07-14
APPLICATION NOMBER: PCT/USvs/18824
FILING DATE: 1998-09-10
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 FILING DATE: 199-09-01
APPLICATION & Makk: PCI/US99/20594
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No. 150:8: PCT/USDE/14552
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 11.2571/50
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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DR FILING DATE: 1998-09-24
DR AFPLICATION NUMBER: 60/106032
DR FILING DATE: 1998-10-28
DR FILING DATE: 1998-11-20
DR FILING DATE: 1999-11-20
DR APPLICATION NUMBER: 60/105778
DR FILING DATE: 1999-03-23
DK APPLICATION NUMBER: 60/135695
DK FILING DATE: 1999-06-15
DK APPLICATION NUMBER: 60/145070
DK APPLICATION NUMBER: 60/145070
DK APPLICATION NUMBER: 60/145090
DK FILING DATE: 1999-07-20
DK APPLICATION NUMBER: 60/145090
DK FILING DATE: 1999-07-26
DK APPLICATION NUMBER: 60/145090
DK APPLICATION NUMBER: 60/145090
DK FILING DATE: 1999-08-17

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 US-03-762-027-4 (1-388) x US-09-870-574-3 (1-325)
 Percent Similarity:
Best Local Similarity:
Query Match:
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 : ILENGTH: 325
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 US-1:-762-027-4 (1-388) x US-10-066-500-137 (1-325)
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 A:PLICANI: Wood, william 1.

I:ILE OF INVENTION: INTERLEUKIN-22 POLYPEPIIDES, NUCLEIC ACIDS ENCLENT

I:ILE OF INVENTION: THE SAME AND METHODS FOR THE TREATMENT OF PARCHEAIT LISTFUERS

ELLE REFERENCE: P2806-1(US)

CURRENT APPLICATION NUMBER: US/09/870,574

CURRENT FILING DATE: 2001-05-30

PHOOR APPLICATION NUMBER: US 60/169,495

HHOOR APPLICATION NUMBER: PCT/US00/14042

FHOR FILING DATE: 2000-05-22

FHOR APPLICATION NUMBER: PCT/US00/23328

FHOR APPLICATION NUMBER: PCT/US00/23328

FHOR FILING DATE: 2000-08-24
 GENERAL INFORMATION:
 Sequence 3, Application US/09870574 Patent No. US20020102723A1
 N. MBER OF SEQ ID NOS:
SE, ID NO 3
LENGTH: 325
 A: PLICANT:
 AI PLICANT:
 A. PLICANF: Gurney, Austin L.
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 223 ValAlaValIleLeuMetAlaSerValPheMetValCysLeuAlaLeuLeuGlyCysPhe 212
 371 GAUGUAAAGAAGCTG-----AAGTGCTACATAAGAIUU1IGIUUIIUAIAAUIUICAGA 324
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325 AGCTGCAGATTCTGTATA 342
 325 AGCIGCAGAITCTGTAIA 342
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 Aggarwal, Sudeepta
Nie, Ming-Hong
Maruoka, Ellen M.
Foster, Jessica S.
 Goddard, Audrey
 8.4
58.50
43.94%
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